Human DNase I

```
PRI
                                                               06-MAR-1995
                         1039 bp
                                    mRNA
            HUMDNASEI
LOCUS
            Human DNase I mRNA, complete cds.
DEFINITION
            M55983
ACCESSION
            M55983.1 GI:181623
VERSION
KEYWORDS
            DNase I.
            Human pancreus, cDNA to mRNA.
SOURCE
            Homo sapiens
  ORGANISM
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 1039)
REFERENCE
            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  AUTHORS
            Recombinant human DNase I reduces the viscosity of cystic fibrosis
  TITLE
            sputum
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  JOURNAL
  MEDLINE
            91067672
                     Location/Qualifiers
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                      VEVMLK"
                      160..1008
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                                   282 g
                                            226 t
BASE COUNT
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        61 ttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag
       121 cattetegte atetetgagg acateaceat cateteagga tgaggggeat gaagetgetg
       181 ggggcgctgc tggcactggc ggccctactg cagggggccg tgtccctgaa gatcgcagcc
       241 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt
       301 gtgcagatcc tgagccgcta tgacatcgcc ctggtccagg aggtcagaga cagccacctg
       361 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac
       421 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg
       481 cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg
       541 aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccggtt cacagaggtc
       601 agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac
       661 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg
       721 atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc
       781 ctgtggacaa gccccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca
       841 cccacgcact gtgcctatga caggategtg gttgcaggga tgctgeteeg aggegeegtt
       901 gttcccgact cggctcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg
       961 gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc
      1021 cacaccagtt gaactgcag
   11
```

Fig. 1

Human DNase I construct

```
06-MAR-1995
                                    mRNA
                                                     PRT
            MHDNASE.DN
                          783 bp
LOCUS
           Human DNase I mRNA, complete cds, Mature sequence modified to remove Nar1
DEFINITION
site
            M55983
ACCESSION
            g181623
NID
            DNase I.
KEYWORDS
            Human pancreus, cDNA to mRNA.
SOURCE
  ORGANISM
            Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 1039)
REFERENCE
            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  AUTHORS
            Recombinant human DNase I reduces the viscosity of cystic fibrosis
  TITLE
            sputum
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  JOHRNAL.
            91067672
  MEDLINE
                     Location/Qualifiers
FEATURES
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                     /clone="hDNase-18-1"
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                     160. .225
     sig peptide
                      /gene="DNase I"
                      160. .1008
     CDS
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                      EDVMLMGDFNAGCSYVRPSQWSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAG
                     MLLRGAVVPDSALPFNFQAAYGLSDQLAQAISDHYPVEVMLK"
                      160. .1008
     gene
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                                   220 g
                                            159 t
                168 a
BASE COUNT
ORIGIN
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       61 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
      121 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
      181 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
      241 CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
      301 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
       361 CGGTTCACAG AGGTCAGGGA GTTTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGGACGCA
       421 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
       481 GAGGACGTCA TGTTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG
       541 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
       601 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
       661 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC
      721 CTGAGTGACC AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG
       781 TGA
//
```

Fig. 2(A)

Description and American Company of the American Company of the American Company of the Company

11

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SYN
                                                               29-AUG-2000
                          858 BP SS-DNA
LOCUS
            PAS155 GB.
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
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                     <10..>75
     frag
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                     <10..>75
     source
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                     /db_xref="taxon:9606"
                     /clone="hDNase-18-1"
                      /tissue_type="pancreas [Split]"
                     10..75
     sig peptide
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                      /codon_start="1"
                      /product="DNase I"
                      /db_xref="PID:g181624"
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LFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPG
                      D... [Split]"
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                      76..858
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      frag
                      /note="1 to 72 of 103linker [Split]"
                      join(76..>126,<127..>129,<131..147)
      frag
                      /note="1 to 78 of 102linker [Split]"
                                                        0 OTHER
                                   251 G
                                             170 T
                          260 C
                 177 A
BASE COUNT
ORIGIN
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        61 CAGGGGGCCG TGTCCCTGAA GATCGCAGCC TTCAACATCC AGACATTTGG GGAGACCAAG
       121 ATGTCCAATG CCACCCTCGT CAGCTACATT GTGCAGATCC TGAGCCGCTA CGACATCGCC
       181 CTGGTCCAGG AGGTCAGAGA CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAACCTC
       241 AATCAGGACG CACCAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC
       301 TATAAGGAGC GCTACCTGTT CGTGTACAGG CCTGACCAGG TGTCTGCGGT GGACAGCTAC
       361 TACTACGATG ATGGCTGCGA GCCCTGCGGG AACGACACCT TCAACCGAGA GCCAGCCATT
       421 GTCAGGTTCT TCTCCCGGTT CACAGAGGTC AGGGAGTTTG CCATTGTTCC CCTGCATGCG
       481 GCCCCGGGGG ACGCAGTAGC CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA
       541 GAGAAATGGG GCTTGGAGGA CGTCATGTTG ATGGGCGACT TCAATGCGGG CTGCAGCTAT
       601 GTGAGACCCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCCCCACCTT CCAGTGGCTG
       661 ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCACT GTGCCTATGA CAGGATCGTG
       721 GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT GTTCCCGACT CGGCTCTTCC CTTTAACTTC
       781 CAGGCTGCCT ATGGCCTGAG TGACCAACTG GCCCAAGCCA TCAGTGACCA CTATCCAGTG
       841 GAGGTGATGC TGAAGTGA
```

Fig. 2(B)

pAS6 - light chain

```
18-AUG-1998
                          721 bp
LOCUS
            HMFG1LC2.D
            HUMANISED HMFG1 LIGHT CHAIN Vnp LEADER.
DEFINITION
ACCESSION
KEYWORDS
SOURCE
  ORGANISM
              (BASES 1 TO 342)
REFERENCE
            VERHOEYEN ET AL
  AUTHORS
            CONSTRUCTION OF RESHAPED HMFG1 ETC
  ጥፐጥፒድ
            IMMUNOL. (1993):78, 364-370
  JOURNAL
            SCANNED IN FROM JOURNAL
COMMENT
FEATURES
  SITES
This is the sequence of the HMFG1 light chain gene with the
Vnp leader sequence attached. Translate from
residue 1. Note residue 399 is T > A in all clones leading
to R133 silent mutation (T in Verhoeyen paper)
BASE COUNT
                197 a
                          202 c
                                   182 g
                                            140 t
```

1 ATGGGATGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCGAC
61 ATCCAGATGA CCCAGAGCCC AAGCAGCCTG AGCGCCAGCG TGGGTGACAG AGTGACCATC
121 ACCTGTAAGT CCAGTCAGAG CCTTTTATAT AGTAGCAATC AAAAGATCTA CTTGGCCTGG
181 TACCAGCAGA AGCCAGGTAA GGCTCCAAAG CTGCTGATCT ACTGGGCATC CACTAGGGAA
241 TCTGGTGTGC CAAGCAGATT CAGCGGTAGC GGTAGCGGTA CCGACTTCAC CTTCACCATC
301 AGCAGCCTCC AGCCAGAGGA CATCGCCACC TACTACTGCC AGCAATATTA TAGATATCCT
361 CGGACGTTCG GCCAAGGGAC CAAGGTGGAA ATCAAACGAA CTGTGGCTGC ACCATCTGTC
421 TTCATCTTCC CGCCATCTGA TGAGCAGTTG AAATCTGGAA CTGCCTCTGT TGTGTGCCTG
481 CTGAATAACT TCTATCCCAG AGAGGCCAAA GTACAGTGGA AGGTGGATAA CGCCCTCCAA
541 TCGGGTAACT CCCAGGAGAG TGTCACAGAG CAGGACAGCA AGGACAGCAC CTACAGCCTC
601 AGCAGCACCC TGACGCTGAG CAAAGCAGAC TACGAGAAAC ACAAAGTCTA CGCCTGCGAA
661 GTCACCCATC AGGGCCTGAG CTCGCCCGTC ACAAAGAGCT TCAACAGGGG AGAGTGTTAG
721 A

//

ORIGIN

?

Fig. 3(A)

```
SYN
                                                               29-AUG-2000
                          730 BP SS-DNA
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LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
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     frag
                     /note="1 to 78 of 102linker [Split]"
                         208 C
                                  184 G
                                           140 T
BASE COUNT
                198 A
ORIGIN
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       61 CACTCCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCCAGCGT GGGTGACAGA
      121 GTGACCATCA CCTGTAAGTC CAGTCAGAGC CTTTTATATA GTAGCAATCA AAAGATCTAC
      181 TTGGCCTGGT ACCAGCAGAA GCCAGGTAAG GCTCCAAAGC TGCTGATCTA CTGGGCATCC
      241 ACTAGGGAAT CTGGTGTGCC AAGCAGATTC AGCGGTAGCG GTAGCGGTAC CGACTTCACC
      301 TTCACCATCA GCAGCCTCCA GCCAGAGGAC ATCGCCACCT ACTACTGCCA GCAATATTAT
      361 AGATATCCTC GGACGTTCGG CCAAGGGACC AAGGTGGAAA TCAAACGAAC TGTGGCTGCA
      421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT
      481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
      541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
      601 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
      661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
      721 GAGTGTTAGA
11
```

Fig. 3(B)

HMFG-1 light chain with Vnp Leader (shaded)

MGWSCIILFLVATATGVHSDIQMTQSPSSLSASVGDRVTITCKSSQSL LYSSNQKIYLAWYQQKPGKAPKLLIYWASTRESGVPSRFSGSGSGT DFTFTISSLQPEDIATYYCQQYYRYPRTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV TEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC

Fig. 3(C)

pAS6 - heavy chain

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14-AUG-1998
                         1404 bp
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LOCUS
DEFINITION _
            HUMANISED HMFG1 heavy chain
ACCESSION
           HHMFG1.H
KEYWORDS
SOURCE
  ORGANISM
REFERENCE
  AUTHORS
            VERHOEYEN ET AL
            CONSTRUCTION OF RESHAPED HMFG1 etc
  TITLE
            IMMUNOL. (1993):78, 364-370
  JOURNAL
            VH domain SCANNED IN FROM JOURNAL
COMMENT
            AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES
            Residue 963 is G > T leading to silent mutation in all clones
FEATURES
  SITES
                                  379 g
                                           253 t
                333 a
                         439 c
BASE COUNT
                 ?
ORIGIN
                                  LEADER
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       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACAFGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
       781 TTCCTCTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
      841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
      901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
      961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
     1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
     1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
     1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
     1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
     1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
     1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
     1381 CTCTCCCTGT CTCCGGGTAA ATGA
                                          Antibody DNase Fusions Made Here
                                         (eg pAS34----39.)
         End of lower hinge region of heavy chain. PAPE Amino
          Acid Seq. Fab'2 fusions were made at this point.
          Those with HYBRID HINGES are altered further
                     GACAAAACTGACACA
          This part
                        K
                           T H
```

After this sequence you get the HYBRID HINGE + LINKER SEQUENCES Then DNAse I (eg Fab-DNase construct pAS302)

Fig. 3(D)

Oligos involved in the fusion of whole antibody-DNase

Fig. 4(A)

Constructs pAS34/37

GAG AGG GAC AGA GGG AGC GGG CTG AAG ATC GCA GCC TTC AAC

L S L S P G K G S G G C G C TT TAG

L S L S P G K G S G G C TT T A A F N z hn DNAse I HMFC-1 AS80 AS79

Constructs pAS35/38

AAA GGG AGC GGC CTG AAG ATC GCA GCC TTC AAC TTT CCC TCG CCG CCC GAC TTC TAG ш Ø ΔG (deletion) CCG GAG AGG GAC AGA GGC L S L S P AS82 AS81

Constructs pAS36/39

GGG AGC GGG CTG AAG ATC GCA GCC TTC AAC CCC TCG CCC GAC TTC TAG L K I A A F N AG (deletion) CCG GAG AGG GAC AGA GGC L S L S P AS84 AS83

Oligos involved in the fusion of Fab'2-DNaseI

Constructs pAS23/27

GCA CCT GAA GGG AGC GGG GGG CTG AAG ATC GCA GCC TTC AAC GGT GGT CGT GGA CTT CCC TCG CCG CCC GAC TTC TAG

P P C P A P E | G S G G L K I A A F N AS74 AS73

LINKER

HMFG1 HINGE

hu DNAse I

ASS GGC GGC GGC CTG AAG ATC GCA GCC TTC AAC ASS 7 GGT GGT CGT GGA CTT TAG ASS 8 GGT CGT GGA CTT CAG ASS 9 GGT GGT GGT GGG CTG AAG ATC GCA GCC TTC AAC ASS 9 CTG TTT TGA GTG TGT ACG ACA GGT GGT GGT GGT CCA GGT GGT CCA GGT GGT CGT GGT CCA GGT GGT CTC ACA ASS 9 CTG TTT TGA GTG TGT ACG ACA GGT GGT GGT CCA GGT GGT CCA GGT GGT CCA GGT GGT CTC ACA ASS 9 CTG TTT TGA GTG TGT ACG ACA GGT GGT GGT CCA GGT GGT CCA GGT GGT CTC ACA ASS 9 CTG TTT TGA GTG TGT ACG ACA GGT GGT CCA GGT GGT CCA GGT GGT CTC ACA ASS 9 CTG TTT TGA GTG TGT ACG ACA GGT GGT CCA GGT GGT CCA GGT GGT CTC ACA ASS 9 CTG TTT TGA GTG TGT ACG ACA GGT GGT CCA GGT GGT GGT CCA GGT GGT GGT CCA GGT GGT GGT CCA GGT GGT GGT CCA GGT GGT GGT CCA GGT GGT GGT CCA GGT GGT GGT CCA GGT GGT GGT CCA GGT GGT GGT CCA GGT GGT GGT CCA GGT GGT GGT GGT GGT GGT GGT GGT GGT GG	n			1	! !	 	1	1	! !			1	1 1 1	! !												
GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC A P E G G L K I A A F N Linker T C C V E C P P C P GG GGG GGG GGG TTC TAG GAG TGT CCA GGG GGG GGG GGG GGG GGG TABBRID HINGE T C C V E C P P C P A B C GG GGG GGG G TGT CCA GGG GGG GGG GGG GGG GGG GGG T C C V E C P P C P A B C GG GGG GGG GGG T C C V E C P P C P A B C GG GGG GGG GGG T C C V E C P P C P A B C GG GGG GGG GGG GGG GGG GGG GGG GGG		ucts pl	AS101	/105	10 1																					
inge) Linker GAG TGT CCA CCG TGT CCA GCA GAG GGG AGC GGC TGT CCA CCG TGT CCA GGT CGT CTC CCC TCG T C C V E C P P C P A P E G S G HYBRID HINGE G TGT CCA GCG TGT CCA GGG GGG GGG GGG T C C V E C P P C P A P E G S G T C C V E C P P C P A P E G S G T C C V E C P P C P A P E G S G T C C V E C P P C P A P E G S G T C C V E C P P C P A P E G S G T C C V E C P P C P A P E G S G T C C V E C P P C P A P E G S G T C C V E C P P C P A P E G S G T C C V E C P P C C P A P E G G T C C V E C P P C C C G G C C C G T C C V E C P P C C C G G C C C G T C C V E C P P C C C C G G C C C G G C C C C G G C		GGT GC	SC AC	3G GG	ST C	CA CGT GT GA	CT G		36C 36C 6			AAG TTC K	ATC TAG I	GCA (3CC	rrc . F	AAC N									
G TGT ACG ACA CAG TGT CCA CCG TGT CCA GCA GCA GGG GGG GGC T C C V E C P P C P A P E G S G HYBRID HINGE G TGT ACG ACA GGT GGC GCG GGG GGG GGG T C C V E C P P C P A P E G S G T C C V E C P P C P A P E G S G T C C V E C P P C P A P E G S G T C C V E C P P C P A P E G S G T C C V E C P P C P A P E G S G T C C V E C P P C P A P E G S GG GGG GGG T C C V E C P P C P A P E G G GG GGG GGG T C C V E C P P C P A P E G G GG GGG GGG GGG T C C V E C P P C P A P E G G GG GGG GGG GGG GGG GGG GGG GGG	•		HMEG	31 (F	Hing	(e)			Sho	rt ker			hu	DNAs	⊢		.									
G TGT ACG ACA CAG TGT CCA GCA GCA GCA GGG GGG AGC GGC T C C V E C P P C P A P E G S GG HYBRID HINGE G TGT ACG ACA GGT GGT GGT GGT GGT GGT TINKE G TGT ACG ACA GGT GGT GGT GGT GGT GGT GGT GGG GGG TGT T C C V E C P P C P A P E G S GG TGT T C C V E C P P C P A P E G GG GGG TGT T C C V E C P P C P A P E G GG GGG TGT T C C V E C P P C C GGT GGT GGT GGT GGT GGT GGG GGG TGT T C C V E C P P C P A P E G GG GGG TGT	нΙ	ucts pi	AS102	:/10(ωı																					
T C C V E C P P C P A P E G S G HYBRID HINGE Long Linke G TGT GAG TGT CCA CCG TGT CCA GCA GGT GGT GGT TT T C C V E C P P C P A P E G G GT TT T C C V E C P P C P A P E G G TT T C C V E C P P C P A P E G G TT T C C V E C P P C P A P E G G TT T C C V E C P P C P A P E G G TT		CTG T	TT TG		IG I	GT	ACG 7	ACA (CAG	GAG CTC			299 922	TGT	CCA	SCA	CCA	GAG	999	AGC	299	999	CTG	AAG	ATC	GCA
G TGT ACG ACA CAG TGT CCA GGT GGT GGT GGT GGT TGT TGT TGT TGT TG		Ω,	T. T		H	E	<u>U</u>	ပ	>	[13]	ပ	щ	Д	ပ	ы	А	Ъ	EJ.	ro	ഗ	დ	Ŋ	ı	×	н	Ø
G TGT ACG ACA CACA GGT GGT CCT GGT CTC CCG TGT CTC TGT CTC CT GGT CTC CCG TGT CTC CTC	•		HMFG1			1						HYBR	H QI	INGE				_						7	ıu Dî	NAse
GTC GAG TGT CCA GCA CCA GAG GGC GGG CTG CAG CTC ACA GGT GGT CGT GGT CTC CCG V E C P A P E G G G L	~ !	ucts p	AS103	3/10.	7														Ä	bud	Link	er				
$\begin{array}{cccccccccccccccccccccccccccccccccccc$; ;	; ;	, ,	{ F	E	, (Ę	GTC	SAG	TGT	CCA	CCG	TGT	CCA	GCA	CCA	GAG	299	999		AAG	ATC	GCA	၁၁၅	TTC
		CTG T	Tr Te K	P P	T. D. H.	<u>7</u> 5 ⊟	<u>ာ</u> ညီ ပ	L L L L	CAG V	E E	ACA	7 0.7 0.5 0.5	GGC P	S C	т Б С		ים ל פ) H	} 5		н	×	H	А	Ą	[±4

ATC GCA GCC TTC

Ø

Hu DNAse I

Short

Hybrid Hinge

HMFG1

pAS23

mRNA

PRI

06-MAR-1995

1554 bp

PAS23.DNA

LOCUS

```
Humanised HMFG1 Fab'2 fused to human DNase I (construct 1)
DEFINITION
ACCESSION
NID
KEYWORDS
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            DNase I sequence is from assembled oligos (thus modified c/f
SOURCE
MHDNASE1.dna)
  ORGANISM
           Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  AUTHORS
            Recombinant human DNase I reduces the viscosity of cystic
  TITLE
fibrosis
            sputum
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  JOURNAL
  MEDLINE
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Fig. 5(A)

with the state of the state of

11

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ACCESSION
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SOURCE
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                344 A
                         466 C
                                           309 T
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      841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
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Fig. 5(B)

11

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     frag
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                     join(730..>744,<745..795)
     frag
                     /note="1 to 78 of 102linker [Split]"
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                                  437 G
                                           309 T
                345 A
BASE COUNT
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       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCGGCGGG
      781 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
      841 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
      901 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
      961 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
     1021 CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
     1081 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
     1141 CGGTTCACAG AGGTCAGGGA GTTTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGGACGCA
     1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
     1261 GAGGACGTCA TGTTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG
     1321 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
     1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
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     1561 TGA
```

Fig. 5(C)

27 36 45 18 ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC --- --- --- --- --- --- --- --- --- --- --- --- ---G W S C I I L F L V A T A T G V H 72 31 90 63 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA S Q V Q L V Q S G A E V K K P G A 153 135 144 126 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---V K V S C K A S G Y T F S A Y W I E 189 198 207 180 171 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT W V R Q A P G K G L E W V 261 252 234 243 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT S N N S R Y N E K F K G R V T V T 306 297 288 279 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---R D T S T N T A Y M E L S S L R S E 369 378 351 360 333 342 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC --- --- --- --- --- --- --- --- --- --- --- --- --- ---Y D F A W F A R S 396 405 414 423 387 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG --- --- --- --- --- --- --- --- --- --- --- --- --- ---W G Q G T L V T V S S A S T K G 477 459 468 450 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG V F P L A P S S K S T S G G T A 495 504 513 522 531 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA G C L V K D Y F P E P V T V S W N S 567 585 576 558 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA L T S G V H T F P A V L Q S S G

Fig. 5(D) (Sheet 1 of 3)

603 612 621 630 639 648 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG --- --- --- --- --- --- --- --- --- --- --- --- ---Y S L S S V V T V P S S S L G T 702 657 666 675 684 693 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAA AAA T Y I C N V N H K P S N T K V D K K 720 729 738 747 756 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT E P K S C D K T H T C P P C P A 792 765 774 783 801 GAA GGG AGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG E G S G G L K I A A F N I Q T F G E 819 828 837 846 ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC K M S N A T L V S Y I V Q I L S R 882 891 900 909 TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG DIALVQEVRDSHLTAVG 927 936 945 954 963 972 AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC K L L D N L N Q D A P D T Y H Y V V 1008 981 990 999 1017 1026 AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG ___ S E P L G R N S Y K E R Y L F V Y R 1035 1044 1062 1071 1080 1053 CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC P D Q V S A V D S Y Y Y D D G C E P 1098 1107 1116 TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG C G N D T F N R E P A I V R F F S R 1152 1161 1170 1179 1143 TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC ___ ___ ___ T E V R E F A I V P L H A A P G D 1206 1215 1224 1233 1242 1197

Fig. 5(D)
(Sheet 2 of 3)

GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA A V A E I D A L Y D V Y L D V Q E K 1269 1278 1287 1260 TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT G L E D V M L M G D F N A G C S Y 1323 1332 1341 1305 1314 GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG V R P S Q W S S I R L W 1377 1386 1395 1368 1359 TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT 1422 1431 1440 1413 CAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG D R I V V A G M L L R G A V V P D S 1503 1485 1494 GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA --- --- --- --- --- --- --- --- --- --- --- --- --- ---L P F N F Q A A Y G L S D Q L A Q 1530 1539 1548 GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' S D H Y P V E V M L K *

Fig. 5(D) (Sheet 3 of 3)

11

pAS27

mRNA

1584 bp

PAS27.DNA

PRI

06-MAR-1995

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  ORGANISM Homo sapiens
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  AUTHORS
            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  TITLE
            Recombinant human DNase I reduces the viscosity of cystic fibrosis
            sputum
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
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Fig. 6(A)

11

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        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GGAGCGGCGG GCTGAAGATC
      781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
      841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
      901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
      961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCGTG
     1021 TACAGGCCTG ACCAGGTGTC TGCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
     1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCTTCTC CCGGTTCACA
     1141 GAGGTCAGGG AGTTTGCCAT TGTTCCCCTG CATGCGGCCC CGGGGGACGC AGTAGCCGAG
     1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
     1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC
     1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
     1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
     1441 GCCGTTGTTC CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
     1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GGGGGGCGGA
     1561 CCCAAAAAGA AGCGCAAGGT TTGA
```

Fig. 6(B)

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29-AUG-2000
            FDDNASE27K 1593 BP SS-DNA
                                                    SYN
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
FEATURES
                     Location/Qualifiers
                     10..1593
                     /note="1 to 1584 of FdDNase27correct"
                     join(10..>729,<796..1593)
     frag
                     /note="1 to 1584 of 27.dna [Split]"
                     730..795
     fraq
                     /note="1 to 66 of 23/27linker"
     frag
                     join(730...>744,<745...795)
                     /note="1 to 78 of 102linker [Split]"
                                  449 G
                                           311 T
BASE COUNT
ORIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCGGCGGG
      781 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
      841 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
      901 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
      961 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
     1021 CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
     1081 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
     1141 CGGTTCACAG AGGTCAGGGA GTTTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGGACGCA
     1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
     1261 GAGGACGTCA TGTTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG
     1321 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
     1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
     1441 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC
     1501 CTGAGTGACC AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG
     1561 GGGGGGGAC CCAAAAAGAA GCGCAAGGTT TGA
11
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Fig. 6(C)

2.7 5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---M G W S C I I L F L V A T A T G V H TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA S Q V Q L V Q S G A E V K K P G A S GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG V K V S C K A S G Y T F S A TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT W V R Q A P G K G L E W V G E I L P GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT G S N N S R Y N E K F K G R V T V AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG D T S T N T A Y M E L S S L R S E GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC ___ ___ ___ A V Y Y C A R S Y D F A W F A Y TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG T L V T V S S A S T K G P GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA G C L V K D Y F P E P V T V S W N S GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA G A L T S G V H T P A V L Q S S G

Fig. 6(D) (Sheet 1 of 3)

612 621 630 639 648 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG L Y S L S S V V T V P S S S L G T Q 666 675 684 693 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA ___ ___ ___ T Y I C N V N H K P S N T K V D K K 720 729 738 747 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT ___ V E P K S C D K T H T C P P C P A P 774 783 792 GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG E G S G G L K I A A F N I Q T F G E 837 855 846 819 828 ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC K M S N A T L V S Y I V Q I L S R 909 873 882 891 900 TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG L V Q E V R D S H L T A V G Y D I A 927 936 945 954 963 AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC L L D N L N Q D A P D T Y H Y V 1017 999 1008 990 AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG S E P L G R N S Y K E R Y L F V Y R 1053 1044 1062 1071 1035 CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC P D Q V S A V D S Y Y Y D D G C E P 1098 1107 1116 1125 TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG C G N D T F N R E P A I V R F F S R 1143 1152 1161 1170 1179 1188 TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC $\begin{smallmatrix} F \end{smallmatrix} \quad T \quad E \quad V \quad R \quad E \quad F \quad A \quad I \quad V \quad P \quad L \quad H \quad A \quad A \quad P \quad G \quad D$ 1197 1206 1215 1224 1233 1242

Fig. 6(D) (Sheet 2 of 3)

GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA A V A E I D A L Y D V Y L D V Q E K 1260 1269 1278 1287 TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT $\hbox{\tt W} \hbox{\tt G} \hbox{\tt L} \hbox{\tt E} \hbox{\tt D} \hbox{\tt V} \hbox{\tt M} \hbox{\tt L} \hbox{\tt M} \hbox{\tt G} \hbox{\tt D} \hbox{\tt F} \hbox{\tt N} \hbox{\tt A} \hbox{\tt G} \hbox{\tt C} \hbox{\tt S} \hbox{\tt Y}$ 1323 1332 1341 1305 1314 GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG R P S O W S S I R L W T S P 1377 1386 1395 1404 1359 1368 TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT ___ ___ __ __ __ __ __ __ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ W L I P D S A D T T A T P T H C A Y 1440 1449 1431 1422 GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG R I V V A G M L L R G A V V P D S 1485 1494 1503 1467 1476 GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA A L P F N F Q A A Y G L S D Q L A Q 1530 1539 1548 1557 1566 1521 GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA I S D H Y P V E V M L K G G P K 1575 1584 AAG AAG CGC AAG GTT TGA 3' --- --- --- ---

Fig. 6D
(Sheet 3 of 3)

pAS34

PAS34.DNA 2196 bp 2196 bp 2196 bp DNA LOCUS HUMANISED HMFG1 heavy chain fused to human DNAse construct 34 DEFINITION DEFINITION Clone 16.4.2 (same as hcdnase1.dna template file) REFERENCE **AUTHORS** VERHOEYEN ET AL CONSTRUCTION OF RESHAPED HMFG1 etc TITLE **JOURNAL** IMMUNOL. (1993):78, 364-370 Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) COMMENT The fusion was made using overlapping oligos AS79 and AS80 AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES** Residue 963 is G > T leading to silent mutation in all clones **FEATURES** SITES Note 677 c 607 q 411 t 501 a BASE COUNT ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CTCCGGGTAA A**GGGAGCGGC GGG**CTGAAGA TCGCAGCCTT CAACATCCAG 1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG 1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG 1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCAGTGAG 1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAGGTG 1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC 1741 AACCGAGAGC CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC 1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC 1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC 1921 AATGCGGGCT GCAGCTATGT GAGACCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC 1981 CCCACCTTCC AGTGGCTGAT CCCCGACAGC GCTGACACCA CAGCTACACC CACGCACTGT 2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG 2101 GCTCTTCCCT TTAACTTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC 2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGTGA

Fig. 7(A)

11

27 36 45 54 9 18 5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC $\begin{smallmatrix} M & G & W & S & C & I & I & L & F & L & V & A & T & A & T & G & V & H \\ \end{smallmatrix}$ TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA --- --- --- --- --- --- --- --- --- --- --- --- ---, S Q V Q L V Q S G A EVKKPGAS 117 126 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT W V R Q A P G K G L E W V G E I GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT S N N S R Y N E K F K G R V T V T AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG R D T S T N T A Y M E L S S L R S E GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC T A V Y Y C A R S Y D F A W F A Y TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG W G Q G T L V T V S S A S T K G P S GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA C L V K D Y F P E P V T V S W N S GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA A L T S G V H T F P A V L Q S S G CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG L Y S L S S V V T V P S S S

Fig. 7(B) (Sheet 1 of 4)

ale and 1891 F. P. S. H. M. B. Market and S. S. Sandara and S. San

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC ELLGGPSVFLFPPKPKDT CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC L M I S R T P E V T C V V V D V S GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT E D P E V K F N W Y V D G V E V H N GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC $\hbox{\tt A} \quad \hbox{\tt K} \quad \hbox{\tt T} \quad \hbox{\tt K} \quad \hbox{\tt P} \quad \hbox{\tt R} \quad \hbox{\tt E} \quad \hbox{\tt E} \quad \hbox{\tt Q} \quad \hbox{\tt Y} \quad \hbox{\tt N} \quad \hbox{\tt S} \quad \hbox{\tt T} \quad \hbox{\tt Y} \quad \hbox{\tt R} \quad \hbox{\tt V} \quad \hbox{\tt V} \quad \hbox{\tt S}$ GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG V L T V L H Q D W L N G K E Y K C K GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA SNKALPAPIEKTISKA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG G Q P R E P Q V Y T L P P S R D E L ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC $\begin{smallmatrix} T & & K & & N & & Q & & V & & S & & L & & T & & C & & L & & V & & K & & G & & F & & Y & & P & & S & & D \\ \end{smallmatrix}$ 1233 1242 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG I A V E W E S N G Q P E N N Y K T T CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG PVLDSDGSFFLYSKLTV GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG K S R W Q Q G N V F S C S V M H E

Fig. 7(B) (Sheet 2 of 4)

- 2

GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA GGG L H N H Y T Q K S L S L S P G K G 1413 1422 1431 1440 AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG <u>SGG</u> L K I A A F N I Q T F G E T K ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC M S N A T L V S Y I V Q I L S R Y D ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG A L V Q E V R D S H L T A V G K L CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG L D N L N Q D A P D T Y H Y V V S E CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC P L G R N S Y K E R Y L F V Y R P D CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA E V R E F A I V P L H A A P G D A V GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC A E I D A L Y D V Y L D V Q E K W G TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA L E D V M L M G D F N A G C S Y V R 1962 1971 1980 1989 1998 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG P S Q W S S I R L W T S P T F Q W L ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG I P D S A D T T A T P T H C A Y D R Fig. 7(B)

(Sheet 3 of 4)

	2	2061		:	2070		2	2079		:	2088		:	2097		:	2106
ATC	GTG	\mathtt{GTT}	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT
							-									-	
I	V	V	Α	G	M	L	L	R	G	Α	V	V	P	D	S	Α	L
	2	2115		1	2124		2	2133			2142		2	2151		2	2160
CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC
P	F	N	F	Q	Α	A	Y	G	L	S	D	Q	L	A	Q	A	I
	2	2169		2	2178		2	2187		2	2196						
AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3 ′					
S	D	Н	Y	P	V	E	V	M	L	K	*						

Fig. 7(B) (Sheet 4 of 4)

pAS35

LOCUS PAS35.DNA 2193 bp 2193 bp DNA 14-AUG-1998 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNAse construct 35 DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G) REFERENCE **AUTHORS** VERHOEYEN ET AL TITLE CONSTRUCTION OF RESHAPED HMFG1 etc **JOURNAL** IMMUNOL. (1993):78, 364-370 COMMENT Human DNAse sequence is modified as a result of oligo assembly (mhdnase.dna) The fusion was made using overlapping oligos AS81 and AS82 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES** Residue 963 is G > T leading to silent mutation in all clones **FEATURES FEATURES** In 17.12.1 residue 1398 is A > G (silent K to K mutation) SITES Note BASE COUNT 500 a 677 c 606 q 410 t ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CTCCGAAG<mark>GG GAGCGCCGGG</mark> CTGAAGATCG CAGCCTTCAA CATCCAGACA 1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC 1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG 1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA 1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT 1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC 1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTCACAG AGGTCAGGGA GTTTGCCATT 1801 GTTCCCCTGC ATGCGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC 1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT 1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC 1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC 2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT 2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT 2161 GACCACTATC CAGTGGAGGT GATGCTGAAG TGA

Fig. 8(A)

ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC C+C TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA <u>S</u>QVQLVQSGAEVKKPGAS GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG V K V S C K A S G Y T F S A Y W I E TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT W V R Q A P G K G L E W V G E I GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT $\begin{smallmatrix} G & S & N & N & S & R & Y & N & E & K & F & K & G & R & V & T & V & T \\ \end{smallmatrix}$ AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG D T S T N T A Y M E L S S L R S E GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC D T A V Y Y C A R S Y D F A W F TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG W G Q G T L V T V S S A S T K G P S GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA G A L T S G V H T F P A V L Q S S G CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG

Fig. 8(B) (Sheet 1 of 4)

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA 1. I C N V N H K P S N T K V GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT V E P K S C D K T H T C P P C P A P GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC ELLGGPSVFLFPPKPK CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC LMISRTPEVTCVVDVSH GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT E D P E V K F N W Y V D G V E V H N GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC --- --- --- --- --- --- --- --- --- --- --- --- ---A K T K P R E E Q Y N S T Y R 981 990 999 1008 1017 1026 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG V L T V L H Q D W L N G K E Y K C K GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA V S N K A L P A P I E K T I S K A K 1098 1107 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG G Q P R E P Q V Y T L P P S R D E L ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC 1197 1206 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG I A V E W E S N G Q P E N N Y K T T CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG PPVLDSDGSFFLYSKLTV GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG D K S R W Q Q G N V F S C S V M H E Fig. 8(B)

(Sheet 2 of 4)

GÇT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG AAG GGG AGC A L P N H Y T Q K S L S L S P K G S 1413 1422 1431 GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG <u>G G</u> L K I A A F N I Q T F G E T K M TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC S N A T L V S Y I V O I L S R Y D I GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG A L V Q E V R D S H L T A V G K L L GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA D N L N Q D A P D T Y H Y V V S E P CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG LGRNSYKERYLFV GTG TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC V S A V D S Y Y Y D D G C E P C G N GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG D T F N R E P A I V R F F S R F T E GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG E I D A L Y D V Y L D V Q E K W G L GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC 1953 1962 1971 1980 1989 1998 TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC S Q W S S I R L W T S P T F Q W L I CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC D S A D T T A 1 P T H C A Y D R I Fig. 8(B)

(Sheet 3 of 4)

	2	2061		2	2070		:	2079		2	2088		- 3	2097		2	2106
GTG	\mathtt{GTT}	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	\mathtt{GTT}	GTT	CCC	GAC	TCG	GCT	CTT	CCC
V	V	A	G	M	L	L	R	G	Α	V	V	P	D	S	Α	L	₽
	2	2115		2	2124		:	2133		2	2142		2	2151		2	2160
TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC	AGT
F	N	F	Q	Α	A	Y	G	L	S	D	Q	L	Α	Q	Α	I	S
	2	2169		2	2178		- 2	2187									
GAC	CAC	\mathtt{TAT}	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3′						
D	н	Y	P	V	E	V	M	L	ĸ	*							

Fig. 8(B) (Sheet 4 of 4)

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pAS36

LOCUS PAS36.DNA 2190 bp 2190 bp DNA 14-AUG-1998 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNAse - construct 36 DEFINITION Clone 18.24.1 with residue 1392 T > C REFERENCE AUTHORS VERHOEYEN ET AL TITLE CONSTRUCTION OF RESHAPED HMFG1 etc JOURNAL IMMUNOL. (1993):78, 364-370 COMMENT Human DNAse sequence is modified as a result of oligo assembly (mhdnase.dna) COMMENT The fusion was made using overlapping oligos AS83 and AS84 **FEATURES** AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES** Residue 963 is G > T leading to silent mutation in all clones **FEATURES** Residue 1392 T > C silent S to S mutation Note SITES BASE COUNT 498 a 678 c 605 g 409 t ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGCC TCGAGTGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CcCCG<u>GGGAG CGGCGGC</u>CTG AAGATCGCAG CCTTCAACAT CCAGACATTT 1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC 1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGACTGCCGT GGGGAAGCTG 1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG 1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG 1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA 1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT 1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC 1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTCATGT TGATGGGCGA CTTCAATGCG 1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC 1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT 2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT 2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC 2161 CACTATCCAG TGGAGGTGAT GCTGAAGTGA

Fig. 9(A)

27 36 45 . 54 5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---G W S C I I L F L V A T A T G V H TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA S Q V Q L V Q S G A É GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG V K V S C K A S G Y T F S A Y W I E TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT W V R Q A P G K G L E W V G E I L P GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT S N N S R Y N E K F K G R V T V T AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG R D T S T N T A Y M E L S S L R S E GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC T A V Y Y C A R S Y D F A TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG W G Q G T L V T V S S A S T K G P S GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA C L V K D Y F P E P V T V S W N S GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG Y S L S S V V T V P S S S L G T Q

Fig. 9(B) (Sheet 1 of 4)

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT E P K S C D K T H T C P P C P A GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC E L L G G P S V F L F P P K P K D T CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT E D P E V K F N W Y V D G V E V H N GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC A K T K P R E E Q Y N S T Y GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG V L T V L H Q D W L N G K E Y K C K GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA V S N K A L P A P I E K T I S K A GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG G Q P R E P Q V Y T L P P S R D E L ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC T K N O V S L T C L V K G F 1206 1215 1224 1233 1242 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG I A V E W E S N G Q P E N N Y K T T CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG P P V L D S D G S F F L Y S K L T V GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG D K S R W Q Q G N V F S C S V M H E

Fig. 9(B) (Sheet 2 of 4)

1359 1368 1377 1386 1395 1404 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGG AGC GGC A L H N κ Y T Q K S L S L S P \underline{G} S \underline{G} GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC G L K I A A F N I Q T F G E T K M S AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC N A T L V S Y I V Q I L S R Y D I A CTG GTC CAG GAG GTC AGA GAC AGC CAG CTG ACT GCC GTG GGG AAG CTG CTG GAC L V Q E V R D S H L T A V G K L L D AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG N L N Q D A P D T Y H Y V V S E P L GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG G R N S Y K E R Y L F V Y R P D Q V TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG GTC $\begin{smallmatrix} T & F & N & R & E & P & A & I & V & R & F & F & S & R & F & T & E & V \\ \end{smallmatrix}$ AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG I D A L Y D V Y L D V Q E K W G L E 1935 1944 GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG Pig. 9(B)

(Sheet 3 of 4)

	2	2061		2	2070		- 2	2079		- 1	2088		2	2097			2106
GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT	CCC	TTT
V	A	G	M	L	L	R	G	Α	V	V	P	Ď	S	Α	L	₽	F
	2	2115		2	2124			2133		2	2142		2	2151		2	2160
AAC	TTC	CAG	GCT	GCC	\mathtt{TAT}	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC	AGT	GAC
N	F	Q	Α	Α	Y	G	L	S	D	Q	L	Α	Q	Α	I	S	D
	2	2169		2	2178		3	2187									
CAC	\mathtt{TAT}	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3′							
Н	Y	P	V	E	V	M	L	K	*								

Fig. 9(B) (Sheet 4 of 4)

pAS37

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LOCUS
            PAS37.DNA
                         2226 bp
                                        2196 bp 2196 bp DNA
                                                                   14-AUG-
1998
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNAse construct 37
DEFINITION Clone 16.4.2 (same as hcdnase1.dna template file) plus NLS
REFERENCE
 AUTHORS
            VERHOEYEN ET AL
  TITLE
            CONSTRUCTION OF RESHAPED HMFG1 etc
  JOURNAL
            IMMUNOL. (1993):78, 364-370
COMMENT
            Human DNAse sequence is modified as a result of oligo assembly
(mhdnase.dna)
COMMENT
            The fusion was made using overlapping oligos AS79 and AS80
FEATURES
            AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES
            Residue 963 is G > T leading to silent mutation in all clones
 SITES
            Note
BASE COUNT
                511 a
                         683 с
                                  619 q
                                           413 t
ORIGIN
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
     601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
     661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
     721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
     781 TTCCTCTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
     841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
      901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
      961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
     1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
     1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
     1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
     1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
     1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
     1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
     1381 CTCTCCCTGT CTCCGGGTAA A<u>GGGAGCGGC GGG</u>CTGAAGA TCGCAGCCTT CAACATCCAG
     1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG
     1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG
     1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCAGTGAG
     1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAGGTG
     1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC
     1741 AACCGAGAGC CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC
     1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
     1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC
     1921 AATGCGGGCT GCAGCTATGT GAGACCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC
     1981 CCCACCTTCC AGTGGCTGAT CCCCGACAGC GCTGACACCA CAGCTACACC CACGCACTGT
     2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG
     2101 GCTCTTCCCT TTAACTTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC
     2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGGGGGGGG GACCCAAAAA GAAGCGCAAG
```

Fig. 10(A)

► NLS

2221 **GTTTGA**

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AT	G GG?	9 A TGG	AGC	TGT	18 ATC	ATC	CTC	27 TTC	TTG	GTA	36 GCA	ACA	GCT	45 ACA	GGT	GTC	54 CAC
 _M	- -	 W	s		 I		 L	 F	 L		 А	 Т	 A	 T	 G	 V	 Н
TC	C CAC	63 GTG	CAG	CTG	72 GTG	CAG	TCT	81 GGG	GCA	GAG	90 GTG	AAA	AAG	99 CCT	GGG	GCC	108 TCA
s	Q	V	Q	L	V	Q	s	G	Α	Ε	V	K	K	P	G	Α	S
GT	G AA	117 G GTG		TGC	126 AAG	GCT	TCT	135 GGC	TAC	ACC	144 TTC	AGT	GCC	153 TAC	TGG	ATA	162 GAG
V	K	V	S	С	K	A	s	G	Y	Т	F	S	A	Y	W	I	E
TG	G GTY	171 G CGC		GCT	180 CCA	GGA	AAG	189 GGC	CTC	GAG	198 TGG	GTC	GGA	207 GAG	TTA	TTA	216 CCT
W	V	R	Q	A	P	G	ĸ	G	L	Е	W	v	G	E	I	L	P
GG	A AGʻ	225 r aat		TCT	234 AGA	TAC	ААТ	243 GAG	AAG	TTC	252 AAG	GGC	CGA	261 GTG	ACA	GTC	270 ACT
G	 s	N	N	2	 R	Y	и	Ε	ĸ	F	ĸ	G	 R	v	T		т
		279			288			297			306			315			324
AG	A GAG	C ACA		ACA		ACA	GCC		ATG	GAG		AGC	AGC		AGG	TCT	
R	. D	т	s	т	N	T	Α	Y	M	E	L	s	s	L	R	s	E
		333			342			351			360			369			378
GA	C AC	A GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC
D	T	A	V	Y	Y	С	A	R	s	Y	D	F	Α	W	F	A	Y
TG	G GG	387 C CAA		TOA	396 CTG	GTC	ACA	405 GTC	TCC	TCA	414 GCC	TCC	ACC	423 AAG	GGC	CCA	432 TCG
W	G	Q	G	T	L	v	T	v	s	s	Α	s	T	K	G	P	s
GT	'C TT	,441 CCC CCC		GCA	450 CCC	TCC	TCC	459 AAG	AGC	ACC	468 TCT	GGG	GGC	477 ACA	GCG	GCC	486 CTG
V	 F	P	L	Α	P	s	s	K	s	T	s	G	G	T	Α	Α	L
		495 C CTG	GTC			TAC			GAA			ACG					
		 L			D							T		s			s
		549	;		558			567			576			585			594
		C CTC		AGC					TTC				CTA		TCC	TCA	
		L											r				
CI	AT O	603 C TCC				GTG			GTG			AGC			GGC		648 CAG
	 . Y	 S	L		s		v		 V	 Р		s	s	 L	 G	 Т	Q
		65									684			693			702
		-	•			n /											

Fig. 10(B) (Sheet 1 of 4)

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA Y I C N V N H K P S N T K V D K K GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT E P K S C D K T H T C P P C P A P GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC LLGGPSVFLFPPKPKDT CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC M I S R T P E V T C V V D V S H GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT E D P E V K F N W Y V D G V E V H N GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC K T K P R E E Q Y N S T Y R V V S GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA S N K A L P A P I E K T I S K A K GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC T K N O V S L T C L V K G F Y P S D ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG I A V E W E S N G Q P E N N Y K T T CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG K S R W Q O G N V F S C S V M H E

Fig. 10(B) (Sheet 2 of 4)

1377 1368 1386 1395 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA GGG --- --- --- --- --- --- --- --- --- --- --- --- --- ---1422 1431 1440 1449 AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG <u>SGG</u>LKIAAFNIQTFGETK 1476 1485 1494 1503 ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---M S N A T L V S Y I V Q I L S R Y D 1530 1539 1548 1557 ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG I A L V O E V R D S H L T A V G K L 1584 1593 1602 1611 CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG 1638 1647 1656 1665 1674 CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC P L G R N S Y K E R Y L F V Y R P D 1683 1692 1701 1710 1719 CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG Q V S A V D S Y Y Y D D G C E P C G 1755 1764 1773 1746 AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA N D T F N R E P A I V R F F S R F T 1809 1791 1800 1818 1827 GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA E V R E F A I V P L H A A P G D A V 1863 1872 1881 1845 1854 GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC A E I D A L Y D V Y L D V Q E K W G 1899 1908 1917 1926 1935 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA L E D V M L M G D F N A G C S 1962 1971 1980 1989 1998 1953 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG P S Q W S S I R L W T S P T F Q W L 2007 2016 2025 2034 2043 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG I P D S A D T T A T P T H C A Y D R Fig. 10(B)

(Sheet 3 of 4)

ATC		2061 GTT	GCA		2070 ATG		CTC				2088 GTT			2097 GAC	TCG		2106 CTT
		~															
1	V	V	A	G	М	L	L	R	G	A	٧	V	Р	D	S	А	L
	:	2115		2	2124		2133			2142			:	2151	2160		
CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC
P	F	N	F	Q	Α	Α	Y	G	L	S	D	Q	L	Α	Q	Α	I
	1	2169		1	2178		:	2187		:	2196		:	2205		2	2214
AGT			TAT				GTG								AAA		
AGT			TAT												AAA		
AGT S			TAT Y												AAA K		
	GAC D	CAC H		CCA	GTG	GAG	GTG	ATG	CTG	AAG	GGG	GGC	GGA	ccc		AAG 	AAG
s	GAC D	CAC H 2223		CCA P	GTG	GAG	GTG	ATG	CTG	AAG	GGG	GGC	GGA	ccc		AAG 	AAG
s	GAC D	CAC H 2223	Y	CCA P	GTG	GAG	GTG	ATG	CTG	AAG	GGG	GGC	GGA	ccc		AAG 	AAG

Fig. 10(B) (Sheet 4 of 4)

pAS38

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LOCUS
            PAS38.DNA
                         2223 bp
                                  2193 bp
                                              DNA
                                                              14-AUG-1998 .
           HUMANISED HMFG1 heavy chain fused to human DNAse construct 38 ·
           Clone 17.12.1 with silent K to K mutation (1398 A > G)+NLS
DEFINITION
REFERENCE
 AUTHORS
           VERHOEYEN ET AL
  TITLE
           CONSTRUCTION OF RESHAPED HMFG1 etc
  JOURNAL
           IMMUNOL. (1993):78, 364-370
COMMENT
           Human DNAse sequence is modified as a result of oligo assembly
(mhdnase.dna)
COMMENT
          The fusion was made using overlapping oligos AS81 and AS82
FEATURES
           AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES
           Residue 963 is G > T leading to silent mutation in all clones
FEATURES
           In 17.12.1 residue 1398 is A > G (silent K to K mutation)
BASE COUNT
                510 a
                         683 c
                                  618 a
ORIGIN
       1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
     121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
     181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
     241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
     301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
     361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
     421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
     481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
     541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
   . 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
     661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
     721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
     781 TTCCTCTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
     841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
     901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
     961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
    1021 TGCAAGGTCT CCAACAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
    1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
    1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
```

1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CTCCGAAg<mark>GG GAGCGGCGGG</mark> CTGAAGATCG CAGCCTTCAA CATCCAGACA 1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC 1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG 1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA 1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT 1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC 1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTCACAG AGGTCAGGGA GTTTGCCATT 1801 GTTCCCCTGC ATGCGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC 1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT 1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC 1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC 2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT

Fig. 11(A)

2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT 2161 GACCACTATC CAGTGGAGGT GATGCTGAAG GGGGGCGGAC CCAAAAAGAA GCGCAAGGTT

-NLS

11

2221 <u>TGA</u>

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC M G W S C I I L F L V A T A T G V H TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA --- --- --- --- --- --- --- --- --- --- --- --- ---S Q V Q L V Q S G A E V K K P G A S GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG V K V S C K A S G Y T F S A Y W I E TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT WVRQAPGKGLEWVGEILP GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT S N N S R Y N E K F K G R V T V T AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG D T S T N T A Y M E L S S L R S E GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC Y Y C A R S Y D F A W F A Y TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG G Q G T L V T V S S A S T K G P S GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG F P L A P S S K S T S G G T A A L GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA 567 576 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA G A L T S G V H T F P A V L Q S S G CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG Y S L S S V V T V P S S S L G T Q

Fig. 11(B) (Sheet 1 of 4)

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA TYICNVNHKPSNTKV 711 720 747 756 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT E D P E V K F N W Y V D G V E V H N GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC A K T K P R E E Q Y N S T Y R V V S GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG V L T V L H Q D W L N G K E Y K C K GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA V S N K A L P A P I E K T I S K A K GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG G Q P R E P Q V Y T L P P S R D E L 1143 1152 1161 1170 1179 1188 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---T K N Q V S L T C L V K G F Y P S D ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG P P V L D S D G S F F L Y S K L T V GAC AAG AGC AGG TGG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG D K S R W Q Q G N V F S C S V M H ϵ

Fig. 11(B) (Sheet 2 of 4)

1395 1404 1368 1377 1386 1359 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG AAG GGG AGC P L H N H Y T Q K S L S L S P K G 1413 1422 1431 1440 1449 1458 GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG <u>G G</u> L K I A A F N I Q T F G E T K M 1467 1476 1485 1494 1503 TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC S N A T L V S Y I V Q I L S R Y D I 1530 1539 1548 1557 GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG LVQEVRDSHLTAVGKLL 1584 1593 1602 1611 1620 GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---1629 1638 1647 1656 1665 1674 CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---L G R N S Y K E R Y L F V Y R P D Q 1683 1692 1701 1710 1719 1728 GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC $\begin{smallmatrix} V \end{smallmatrix} \ \ S \ \ A \ \ V \ \ D \ \ S \ \ Y \ \ Y \ \ D \ \ D \ \ G \ \ C \ \ E \ \ P \ \ C \ \ G \ \ N$ 1755 1764 1773 GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG TFNREPAIVRFFSRFTE 1791 1800 1809 1818 1827 GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC V R E F A I V P L H A A P G D A V A 1854 1863 1872 1881 GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG LYDVYLDVQEKW 1908 1917 1926 1899 1935 GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC 1980 1953 1962 1971 1989 TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC SQWSSIRLWTSPTFOWLI 2016 2025 2034 2043 CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC S A D T T A T P T H C A Y D R I

Fig. 11(C) (Sheet 3 of 4)

	2061			:	2070		:	2079		1	2088		2	2097		:	2106	
GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT	CCC	
V	V	Α	G	M	L	L	R	G	Α	V	V	P	D	S	Α	L	₽	
		2115		:	2124			2133		2142			2	2151		2160		
TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC	AGT	
F	N	F	Q	Α	Α	Y	G	L	S	D	Q	L	Α	Q	Α	I	S	
		2169			2178			2187			2196			2205			2214	
GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	GGG	GGC	GGA	CCC	AAA	AAG	AAG	CGC	
D	Н	Y	P	V	E	V	M	L	K	<u>G</u>	G	G	P	K	K	K	R	
												-						
	:	2223										-	 					
AAG		2223 TGA	3′							•								
AAG K			3′							-							-	

Fig. 11(D) (Sheet 4 of 4)

pAS39

LOCUS PAS39.DNA 2190 bp 2220 bp DNA 14-AUG-1998 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNAse - construct 39 DEFINITION Clone 18.24.1 with residue 1392 T > C +NLS REFERENCE AUTHORS VERHOEYEN ET AL TITLE CONSTRUCTION OF RESHAPED HMFG1 etc JOURNAL IMMUNOL. (1993):78, 364-370 COMMENT Human DNAse sequence is modified as a result of oligo assembly (mhdnase.dna) COMMENT The fusion was made using overlapping oligos AS83 and AS84 **FEATURES** AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) Residue 963 is G > T leading to silent mutation in all clones **FEATURES FEATURES** Residue 1392 T > C silent S to S mutation SITES Note BASE COUNT 508 a 684 c 617 g 411 t ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CcCCG<u>GGGAG CGGCGGC</u>CTG AAGATCGCAG CCTTCAACAT CCAGACATTT 1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC 1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGACTGCCGT GGGGAAGCTG 1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG 1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG 1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA 1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT 1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC 1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTCATGT TGATGGGCGA CTTCAATGCG 1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC 1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT 2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT 2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC 2161 CACTATCCAG TGGAGGTGAT GCTGAAGGGG GGCGGACCCA AAAAGAAGCG CAAGGTTTGA

Fig. 12(A)

		9			18			27			36			45			54
ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
M	G	W	s	С	I	I	L	F	L	v	A	Т	А	Т	G	V	н
		63			72			81			90			99			108
TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
s	Q	V	Q	L	V	Q	s	G	A	£	V	K	K	P	G	A	S
		117			126			135			144			153			162
GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
V	K	V	s	С	K	Α	s	G	Y	T	F	s	Α	Y	W	I	E
		171			180			189			198			207			216
TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	TTA	TTA	CCT
W	V	R	Q	A	P	G	ĸ	G	L	E	W	v	G	E	I	L	P
		225			234			243			252			261			270
GGA	AGT	AAT 	AAT 	TCT	AGA	TAC	AAT 	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
G	S	N	N	s	R	Y	N	E	K	F	K	G	R	V	T	V	T
		279			288			297			306			315			324
AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
R	D	т	s	Т	И	T	Α	Y	M	E	L	s	s	L	R	s	E
		333			342			351			360			369			378
GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC
D	T	A	V	Y	Y	С	A	R	S	Y	D	F	A	W	F	Α	Y
		387			396			405			414			423			432
TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG
W	G	Q	G	T	L	V	T	v	s	s	A	s	T	K	G	P	s
		441			450			459			468			477			486
GTC			CTG	GCA	ccc	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC 	ACA	GCG	GCC	CTG
V	F	P	L	Α	P	S	S	K	S	T	S	G	G	T	A	A	L
ccc	TCC	495 CTC	CMC	220	504	ma c	mmc	513	C))	000	522	200	CMC	531 TCG	mcc.	* * C	540
G	С	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	И	S
GGC	GCC	549 CTG	ACC	AGC	558 GGC	GTG	CAC	567 ACC	TTC	CCG	576 GCT	GTC	СТА	585 CAG	TCC	TCA	594 GGA
G	A	L	T	S	G	V	Н	т	F	P	Α	V	L	Q	S	S	G
COC	m x C	603	C.M.C	100	612	C.D.C	CMC	621	cmc	000	630	200	100	639	000	100	648
CTC	TAC	TCC	crc	AGC	AGC	GTG	GTG	ACC	GTG		TCC	AGC	AGC	TTG	GGC 	ACC	CAG
L	Y	s	L	s	S	V	V	Τ	V	P	s	s	s	L	G	Т	Q
		657			666			675			684			693			702

Fig. 12(B) (Sheet 1 of 4)

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA ICNVNHKPSNTK GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT V E P K S C D K T H T C P P GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC LMISRTPEVTCVVDVSH GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT --- --- --- --- --- --- --- --- --- --- --- --- --- ---E D P E V K F N W Y V D G V E V H N 927 936 945 963 972 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC A K T K P R E E Q Y N S T Y R V V S GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG V L T V L H Q D W L N G K E Y K C K GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA --- --- --- --- --- --- --- --- --- --- --- --- ---V S N K A L P A P I E K T I S K A K GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---1152 1161 1170 1179 1188 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC T K N Q V S L T C L V K G F Y P S D ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG I A V E W E S N G Q P E N N Y K T T CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG P P V L D S D G S F F L Y S K L T V GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG D K S R W Q Q G N V F S C S V M F C

Fig. 12(B) (Sheet 2 of 4)

1368 1377 1386 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGG AGC GGC A L H N H Y T Q K S L S L S P <u>G</u> S GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC 1467 1476 1485 1494 1503 1512 AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC N A T L V S Y I V Q I L S R Y D I A CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC V Q E V R D S H L T A V G K L L D AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG G R N S Y K E R Y L F V Y R 1683 1692 1701 TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC S A V D S Y Y Y D D G C E P C G N D ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG I D A L Y D V Y L D V Q E K W G L E GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC 1953 1962 1971 1980 CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC Q W S S I R L W T S P T F Q W L I P GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG D S A D T T A T P T H C A Y D R I V

Fig. 12(B) (Sheet 3 of 4)

. . . .

GTT TGA 3'

Fig. 12(B) (Sheet 4 of 4)

pAS101

```
PAS101.DNA
                                                                         1548 bp
                                                                                                         mRNA
                                                                                                                                                        PRI
                                                                                                                                                                                     06-MAR-1995
                                   Humanised HMFG1 Fab'2 fused to human DNase I (pAS101)
DEFINITION
ACCESSION
NID
KEYWORDS
                                   DNase I.
SOURCE
                                   DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
      ORGANISM
                                  Homo sapiens
                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                   Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      AUTHORS
                                   Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
      TITLE
                                   Recombinant human DNase I reduces the viscosity of cystic
fibrosis
                                   sputum
      JOURNAL
                                   Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
     MEDLINE
                                   91067672
BASE COUNT
                                              343 a
                                                                         467 c
                                                                                                   430 g
                                                                                                                             308 t
ORIGIN
                       1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
                    61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
                 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
                 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
                 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
                 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
                 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
                 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
                 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
                 541 GGCGCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
                 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
                 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
                 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAA\underline{\mathbf{c}} \underline{\mathbf{c}} \underline{\mathbf{c}}
                 781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
                 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
                 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
                 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
              1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
              1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
              1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
              1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
              1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
              1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
              1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
              1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
              1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA
```

Fig. 13(A)

```
LOCUS
            FDDNASE101
                        1548 BP SS-DNA
                                                    SYN
                                                               25-AUG-2000
DEFINITION
ACCESSION
KEYWORDS
SOURCE
FEATURES
                     Location/Qualifiers
                     join(1..>720,<781..1548)
     frag
                     /note="1 to 1548 of PAS101.dna [Split]"
     frag
                     721..780
                     /note="1 to 60 of 101/105linker"
     frag
                     join(721..>735,<736..>759,<760..>780)
                     /note="1 to 80 of 102linker [Split]"
BASE COUNT
                343 A
                         465 C
                                  431 G
                                           309 T
                                                      0 OTHER
ORIGIN
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
     181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
     241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
     541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
     721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC
     781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
     841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
      901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
     961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
     1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
     1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
     1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
     1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
     1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
     1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
    1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
    1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
     1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA
```

Fig. 13(B)

```
LOCUS
            FDDNASE101
                       1557 BP SS-DNA
                                                     SYN
                                                               29-AUG-2000
DEFINITION
ACCESSION
KEYWORDS
SOURCE
FEATURES
                     Location/Qualifiers
     frag
                     10..1557
                     /note="1 to 1548 of FdDNase101correct"
     frag
                     join(10..>729,<790..1557)
                     /note="1 to 1548 of PAS101.dna [Split]"
                     730..789
     fraq
                     /note="1 to 60 of 101/105linker"
                     join(730..>744,<745..>768,<769..>789)
     frag
                     /note="1 to 80 of 102linker [Split]"
                                  433 G
BASE COUNT
                344 A
                         471 C
                                           309 T
                                                       0 OTHER
ORIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
      781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCTCGTC
      841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAGAGAC
      901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
      961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTTC
     1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG
     1081 CCCTGCGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTTC
     1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCGGGGGA CGCAGTAGCC
     1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
     1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA
     1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
     1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
     1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTTAACTTCC AGGCTGCCTA TGGCCTGAGT
     1501 GACCAACTGG CCCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGTGA
```

Fig. 13(C)

27 18 36 ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---M G W S C I I L F L V A T A T G V 81 90 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA S Q V Q L V Q S G A E V K K P G A 117 126 135 144 153 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG V K V S C K A S G Y T F S A Y W I E 180 189 198 207 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---W V R Q A P G K G L E W V G E I L 243 252 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT G S N N S R Y N E K F K G R V T V 288 297 306 315 279 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG R D T S T N T A Y M E L S S L R S E 360 369 333 342 351 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC 396 405 414 387 423 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG W G O G T L V T V S S A S T K G P S 441 450 459 468 477 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG V F P L A P S S K S T S G G T A A 513 495 504 522 531 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA --- --- --- --- --- --- --- --- --- --- --- --- ---549 558 567 576 585 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA G A L T S G V H T F P A V L Q S S G

Fig. 13(D) (Sheet 1 of 3)

CTC	TAC	603 TCC	CTC	AGC	612 AGC	GTG	GTG	621 ACC	GTG	ccc	630 TCC	AGC	AGC	639 TTG	GGC	ACC	64 ⁸ CAG
L	Y	S	L	S	S	V	V	T	V	P	S	S	S	Ĺ	G	Т	Q
		657			666			675			684			693			702
ACC	TAC	ATC	TGC	AAC	GTG	TAA	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	A.A.
T	Y	I	С	N	V	N	Н	К	P	s	N	T	K	V	D	k	K
		711			720			729			738			747			756
GTT	GAG		AAA	TCT		GAC	AAA		CAC	ACA	TGC	CCA	CCG		CCA	GCA	
V	£	P	K	S	С	D	K	T	Н	т	С	P	₽	С	P	A	₽
<i>a</i>	200	765	ama		774		~~~	783			792			801	~.~		810
GAA	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	GGG	GAG	ACC	AAG
E	G	G	L	K	I	A	A	F	N	I	Q	Т	F	G	E	T	K
		819			828			837			846			855			864
ATG	TCC	TAA	GCC	ACC	CTC	GTC	AGC	TAC	TTA	GTG	CAG	ATC	CTG	AGC	CGC	TAC	GAC
M	s	N	A	T	L	v	s	Y	I	v	Q		L L	s	 R	 Y	D
		873			882			001			000			000			010
ATC	GCC		GTC	CAG		GTC	AGA	891 GAC	AGC	CAC	900 CTG	ACT	GCC	909 GTG	GGG	AAG	918 CTG
		т	 V														
7	A	ь	V	Q	E	V	R	Ð	S	Н	L	T	Α	V	G	K	Į,
		927			936			945			954			963			972
CTG	GAC	AAC	CTC	TAA	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC	GTG	GTC	AGT	GAG
L	D	N	L	N	Q	D	Α	P	D	Т	Y	Н	Y	V	V	S	Ε
		981			990			999			1008			1017		-	1026
CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG	TAC	AGG	CCT	GAC
 P	 L	 G	 R		 S	 Y	 К	 E	 R	 Y	 L	 F	 V	 Y	 R	 P	 D
												•				-	
CAG		1035	ccc		1044	አርር		1053	ጥአር		1062 GAT	ccc		071	CCC		080
~																	
Q	V	\$	A	V	D	S	Y	Y	Y	D	D	G	С	Ε	P	С	G
		1089		:	1098		:	1107		:	1116		:	1125		1	1134
	GAC	ACC		AAC	CGA	GAG	CCA	GCC	TTA	GTC	AGG	TTC	TTC	TCC			
	GAC	ACC		AAC	CGA	GAG	CCA	GCC	ATT	GTC		TTC	TTC	TCC		TTC	ACA
	GAC D	ACC	 F	AAC N	CGA R	GAG E	CCA P	GCC A	ATT I	GTC V	AGG R	TTC F	TTC F	TCC S	 R	TTC F	ACA T
N	GAC D	ACC T	F	AAC N	CGA R 1152	GAG G	CCA P	GCC A 1161	ATT I	GTC V	AGG	TTC F	TTC F	TCC S 1179	 R	TTC	ACA T T
N GAG	GAC D GTC	ACC T T 1143 AGG	F GAG	AAC N TTT	CGA R R 1152 GCC	GAG E ATT	CCA P	GCC A 1161 CCC	ATT I CTG	GTC V CAT	AGG R 1170 GCG 	TTC F GCC	TTC F CCG	TCC S 1179 GGG	R GAC	TTC F GCA	ACA T 1188 GTA
N GAG	GAC D GTC	ACC T T 1143 AGG	F GAG	AAC N TTT F	CGA R R 1152 GCC A	GAG E ATT	CCA P GTT V	GCC A 1161 CCC P	ATT I CTG	GTC V CAT H	AGG R R 1170 GCG	TTC F GCC A	TTC F CCG P	TCC S 1179 GGG	R GAC	TTC F GCA A	ACA T 1188 GTA

Fig. 13(D) (Sheet 2 of 3)

GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC D V Q E K W G Y D V 1260 1269 1278 1287 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA L E D V M L M G D F N A G C S Y V R 1305 1314 1323 1332 1341 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG --- --- --- --- --- --- --- --- --- --- --- ---P S Q W S S I R L W T S P T F Q W L 1368 1377 1386 1395 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG I P D S A D T T A T P T H C A Y D R 1413 1422 1431 1440 1449 ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT I V V A G M L L R G A V V P D S A L 1476 1485 1494 1503 CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC F N F Q A A Y G L S D Q L A Q A I 1530 1539 AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' --- --- --- --- --- --- --- --- ---S D H Y P V E V M L K *

Fig. 13(D) (Sheet 3 of 3)

//

pAS102

```
LOCUS
            PAS102.DNA
                          1566 bp
                                     mRNA
                                                      PRI
                                                                06-MAR-1995
            Humanised HMFG1 Fab'2 fused to human DNase I (pAS102)
DEFINITION
ACCESSION
NID
KEYWORDS
            DNase I.
SOURCE
            DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
               (See Figure 2)
  ORGANISM
            Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  AUTHORS
            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  TITLE
            Recombinant human DNase I reduces the viscosity of cystic
fibrosis
            sputum
  JOURNAL
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  MEDLINE
            91067672
BASE COUNT
                345 a
                          469 c
                                   440 g
                                            312 t
ORIGIN
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
```

```
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC
 781 GGCCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
 841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
 901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
 961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC
1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGTGA
```

Fig. 14(A)

```
LOCUS
            FDDNASE102
                       1566 BP SS-DNA
                                                    SYN
                                                               23-MAR-2001
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                345 A
                         468 C
                                  440 G
                                           313 T
                                                      0 OTHER
BASE COUNT
ORIGIN
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGGAGCGGC
      781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
      841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
      901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
      961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
     1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
     1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
     1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
     1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
     1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
     1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC
     1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
     1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTTCCA GGCTGCCTAT
     1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
     1561 AAGTGA
11
```

Fig. 14(B)

pAS302

```
FDDNASE302
LOCUS
                         1575 BP SS-DNA
                                                     SYN
                                                               29-AUG-2000
DEFINITION
ACCESSION
KEYWORDS
SOURCE
FEATURES
                     Location/Oualifiers
     frag
                     10..1575
                     /note="1 to 1566 of FdDNase102correct"
BASE COUNT
                346 A
                                  442 G
                                            313 T
ORIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
      781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTTGGGGA GACCAAGATG
      841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG
      901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT
      961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT
     1021 AAGGAGCGCT ACCTGTTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC
     1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC
     1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAGG GAGTTTGCCA TTGTTCCCCT GCATGCGGCC
     1201 CCGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG
     1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGCGACTTCA ATGCGGGCTG CAGCTATGTG
     1321 AGACCCTCCC AGTGGTCATC CATCCGCCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC
     1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT
     1441 GCAGGGATGC TGCTCCGAGG GGCCGTTGTT CCCGACTCGG CTCTTCCCTT TAACTTCCAG
     1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG
     1561 GTGATGCTGA AGTGA
11
```

Fig. 14(C)

27 45 18 36 5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---MGWSCIILFLVATA 72 81 90 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---SQVQLVQSGAEVKK 117 126 135 144 153 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG V K V S C K A S G Y T F S A Y W I E 171 180 189 198 207 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---WVRQAPGKGLEWVGEILP 234 243 252 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---G S N N S R Y N E K F K G R V T V T 279 288 297 306 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG R D T S T N T A Y M E L S S L R S E 342 351 360 369 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC D T A V Y Y C A R S Y D F A W F A Y 387 396 405 414 423 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG W G Q G T L V T V S S A S T 450 459 468 477 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG P L A P S S K S T S G G 504 513 522 531 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GCLVKDYFPEPVTV 549 558 567 576 585 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA G A L T S G V H T F P A V L Q S Fig. 14(D)

(Sheet 1 of 3)

612 621 630 639 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG Y S L S S V V T V P S S S L G T 702 657 675 684 666 693 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K V D K K 720 738 729 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---V E P K S C D K T H T C C V E C P P 783 792 774 801 TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG PEGSGGLKIAAFNIQ 828 837 846 855 ACA TTT GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG T F G E T K M S N A T L V S Y I V Q 900 909 873 882 891 ATC CTG AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG L S R Y D I A L V Q E V R D S H L 936 945 954 927 963 ACT GCC GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT T A V G K L L D N L N O D A P D T Y 999 1008 1017 981 990 CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---H Y V V S E P L G R N S Y K E R Y L 1035 1044 1053 1062 1071 1080 TTC GTG TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT F V Y R P D Q V S A V D S Y Y Y D D 1098 1107 1116 1125 GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG G C E P C G N D T F N R E P A I V R 1143 1152 1161 1170 1179 TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG ___ ___ ___ ___ F S R F T E V R E F A I V P L H A 1206 1215 1224 1233 1242 1197

Fig. 14(D) (Sheet 2 of 3)

GCC CCG GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT P G D A V A E I D A L Y D V Y L 1251 1260 1269 1278 1287 GTC CAA GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GLEDVML 1314 1323 1332 GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC G C S Y V R P S Q W S S I R L W 1368 1377 1386 1395 CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG --- --- --- --- --- --- --- --- --- --- --- --- ---PTFOWLIPDSADTTATPT 1422 1431 1440 CAC TGT GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT H C A Y D R I V V A G M L L R G A V 1476 1485 1494 1503 GTT CCC GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC 1539 1548 1557 1530 CAA CTG GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' Q L A Q A I S D H Y P V E V M L K *

Fig. 14(D) (Sheet 3 of 3)

LOCUS

11

PAS103.DNA

pAS103

mRNA

06-MAR-1995

1560 bp

```
DEFINITION
            Humanised HMFG1 Fab'2 fused to human DNase I (pAS103)
ACCESSION
NID
KEYWORDS
            DNase I.
SOURCE
            DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
  ORGANISM Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  AUTHORS
            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  TITLE
            Recombinant human DNase I reduces the viscosity of cystic
fibrosis
            sputum
  JOURNAL
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
            91067672
  MEDLINE
BASE COUNT
                344 a
                         468 c
                                  436 q
                                           312 t
ORIGIN
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
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      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCGGG
      781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
      841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
      901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
      961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
     1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
     1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
     1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
     1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
     1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
     1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
     1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
     1441 CGAGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
     1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
```

Fig. 15(A)

```
25-AUG-2000
            FDDNASE103
                       1560 BP SS-DNA
                                                    SYN
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
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     fraq
                     /note="1 to 1560 of PAS103.dna [Split]"
     frag
                     721..792
                     /note="1 to 72 of 103/107linker"
                     join(721..>771,<772..792)
     fraq
                     /note="1 to 78 of 102linker [Split]"
                                           313 T
                                                       0 OTHER
                         467 C
                                  436 G
BASE COUNT
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       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCGGGCTG
      781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
      841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
      901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
      961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
     1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
     1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
     1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
     1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
     1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
     1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
     1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
     1441 CGAGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
     1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
11
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Fig. 15(B)

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FDDNASE103
                       1569 BP SS-DNA
                                                    SYN
                                                              29-AUG-2000
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
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                     /note="1 to 1560 of PAS103.dna [Split]"
     frag
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                     /note="1 to 72 of 103/107linker"
                     join(730..>780,<781..801)
     fraq
                     /note="1 to 78 of 102linker [Split]"
                                  438 G
                                           313 T
                345 A
BASE COUNT
ORIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
      781 GGCGGGCTGA AGATCGCAGC CTTCAACATC CAGACATTTG GGGAGACCAA GATGTCCAAT
      841 GCCACCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG
      901 GAGGTCAGAG ACAGCCACCT GACTGCCGTG GGGAAGCTGC TGGACAACCT CAATCAGGAC
      961 GCACCAGACA CCTATCACTA CGTGGTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG
     1021 CGCTACCTGT TCGTGTACAG GCCTGACCAG GTGTCTGCGG TGGACAGCTA CTACTACGAT
     1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAGGTTC
     1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTTC CCCTGCATGC GGCCCCGGGG
     1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
     1261 GGCTTGGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
     1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
     1381 AGCGCTGACA CCACAGCTAC ACCCACGCAC TGTGCCTATG ACAGGATCGT GGTTGCAGGG
     1441 ATGCTGCTCC GAGGGGCCGT TGTTCCCGAC TCGGCTCTTC CCTTTAACTT CCAGGCTGCC
     1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG
     1561 CTGAAGTGA
//
```

Fig. 15(C)

			9			18			27			36			45			54
A	TG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
-	 M	 G		 S	 C			 L	 F	 L	 V	 A	 Т	 A	 Т	 G	 V	 Н
	r:	G	VV	3	C	1	T	ь	r	L	v	^	1		ı	G	V	11
			63			72			81			90			99			108
Ţ	CC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GC A	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
-	s -	Q		Q			Q	s	 G	 A	 Е	v		к	P	 G	 A	S
	3	Q	V	V	ь	V	V	S	G	7	15	v	10		•	0		5
			117			126			135			144			153			162
G	TG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
-	v			 s			 A	 s	 G	Y	 T	F	s	 A	 Y	 W	 I	E
	•	10	·	5	_	10	**	2	Ü	•	•	•	Ü	••	-	••	_	J
			171			180			189			198			207			216
Т	GG.	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
_	w	 V	 R	0	 A	 P	-		G		 E	w			E			P
		·	••	*		-	J	••	•	_	_			_	_	_	_	_
			225			234			243			252			261			270
G	GA	AGT	TAA	TAA	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
-	 G	s	N	N	 S	R	 Y	n		т	F	К	 G	 R	v	T	v	T
	•	J	•			• •		•	_									
			279			288			297			306			315			324
,2A	.GA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
-	R	D	т	S	T	N	Т	Α	Y	M	Ε	L	s	S	L	Ŕ	S	E
_		202	333	C/D/C	መእመ	342	THO OT	CCA	351	mcc.	መአሮ	360	സസസ	ccc	369 TGG	ሙሙጥ	CCT	378
-		ACA																
	D	Т	Α	V	Y	Y	С	Α	R	S	Y	D	F	A	W	F	A	Y
			202			200			405			41.4			400			422
7	ററാ	GGC	387 CAA	GGG	ACT	396 CTG	GTC	ACA	405 GTC	TCC	TCA	414 GCC	TCC	ACC	423 AAG	GGC	CCA	432 TCG
_																		
	M	G	Q	G	T	L	V	T	V	S	S	Α	S	\mathbf{T}	K	G	P	S
			441			450			459			468			477			486
	STC	TTC		CTG	GCA			TCC		AGC	ACC			GGC		GCG	GCC	CTG
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	Т	Α	A,	L
			495			504			513			522			531			540
(GGC	TGC			A.A.G			TTC			CCG			GTG	TCG		AAC	
															-			
	G	С	L	V	K	D	Y	F	P	Ξ	P	V	T	V	S	M	N	S
			549			558			567			576			585			594
															CAG			
	G	A	L	T	5	G	V	н	1.	r	f.	М	V	Ļ	Q	.>	5	G

Fig. 15(D) (Sheet 1 of 3)

639 612 621 630 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG . Y S L S S V V T V P S S S L G T Q 666 657 675 684 693 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K V D F K 720 729 738 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG --- --- --- --- --- --- --- --- --- --- --- --- --- ---K T H T C C V E C E P K S C D 774 783 792 801 765 TGC CCA GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT PAPEGGLKIAAFNIQTF 828 837 846 855 GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG $\hbox{\tt G} \hbox{\tt E} \hbox{\tt T} \hbox{\tt K} \hbox{\tt M} \hbox{\tt S} \hbox{\tt N} \hbox{\tt A} \hbox{\tt T} \hbox{\tt L} \hbox{\tt V} \hbox{\tt S} \hbox{\tt Y} \hbox{\tt I} \hbox{\tt V} \hbox{\tt Q} \hbox{\tt I} \hbox{\tt L}$ 891 900 909 873 882 AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC Y D I A L V Q E V R D S H L T A 963 927 936 945 954 GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC V G K L L D N L N Q D A P D T Y H Y 1008 999 1017 981 990 GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG $\begin{smallmatrix} V & V \end{smallmatrix} \ \, \mathsf{S} \ \ \, \mathsf{E} \ \ \, \mathsf{P} \ \ \, \mathsf{L} \ \ \, \mathsf{G} \ \ \, \mathsf{R} \ \ \, \mathsf{N} \ \ \, \mathsf{S} \ \ \, \mathsf{Y} \ \ \, \mathsf{K} \ \ \, \mathsf{E} \ \ \, \mathsf{R} \ \ \, \mathsf{Y} \ \ \, \mathsf{L} \ \ \, \mathsf{F} \ \ \, \mathsf{V}$ 1035 1044 1053 1062 1071 1080 TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC R P D Q V S A V D S Y Y Y D D G C 1107 1116 1125 1098 GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC E P C G N D T F N R E P A I V R F F 1170 1179 1188 1152 1161 TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG R F T E V R E F A I V P L H A A P 1215 1206 1224 1233 1242 1197

> Fig. 15(D) (Sheet 2 of 3)

GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA G D A V A E I D A L Y D V Y L D V Q 1260 1269 1278 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC 1314 1323 1332 1341 1305 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC 1368 1377 1386 1395 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT Q W L I P D S A D T T A T P T H C 1422 1431 1440 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC Y D R I V V A G M L L R G A V V P 1476 1485 1494 1503 1467 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG S A L P F N F Q A A Y G L S D Q L 1548 1530 1539 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' Q P I S D H Y P V E V M L K *

Fig. 15(D) (Sheet 3 of 3)

pAS104

mRNA

PRI

06-MAR-1995

```
LOCUS
            PAS104.DNA
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Position 924 G to A by ggg to gag
Linker GR instead of GG (position 777)
NID
KEYWORDS
            DNase I.
            DNase I sequence is from assembled oligos (thus modified c/f
SOURCE
MHDNASE1.dna)
  ORGANISM Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  AUTHORS
            Recombinant human DNase I reduces the viscosity of cystic
  TITLE
fibrosis
            sputum
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  JOURNAL
            91067672
  MEDLINE
                346 a
                         468 c
                                  434 q
                                           312 t
BASE COUNT
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      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
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      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
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      721 GACAAAACTC ACACA<u>TGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCAGG</u>CTG
      781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
      841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
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     1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
     1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
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     1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
     1441 CGAGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
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```

Fig. 16(A)

11

```
LOCUS
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ACCESSION
KEYWORDS
SOURCE
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                     721..792
     frag
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                     /note="1 to 78 of 102linker [Split]"
                         467 C
                                  434 G
                                           313 T
BASE COUNT
                346 A
ORIGIN
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCAGGCTG
      781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
      841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
      901 GACAGCCACC TGACTGCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
      961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
     1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
     1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
     1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
     1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
     1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
     1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
     1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
     1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
     1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
```

Fig. 16(B)

27 1.8 3.6 5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC M G W S C I I L F L V A T A T G V F 90 99 108 72 81 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TC1 S Q V Q L V Q S G A E V K K P G A S 126 135 144 153 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG V K V S C K A S G Y T F S A 189 198 207 171 180 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT W V R Q A P G K G L E W V G E I L P 243 252 261 234 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT $\hbox{\tt G} \quad \hbox{\tt S} \quad \hbox{\tt N} \quad \hbox{\tt N} \quad \hbox{\tt S} \quad \hbox{\tt R} \quad \hbox{\tt Y} \quad \hbox{\tt N} \quad \hbox{\tt E} \quad \hbox{\tt K} \quad \hbox{\tt F} \quad \hbox{\tt K} \quad \hbox{\tt G} \quad \hbox{\tt R} \quad \hbox{\tt V} \quad \hbox{\tt T} \quad \hbox{\tt V} \quad \hbox{\tt T}$ 279 288 297 306 315 AGA GAC ACA TOC ACA AAC ACA GOC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG D T S T N T A Y M E L S S L R S E 351 360 369 342 333 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC A R S Y D F A W F A Y T A V Y Y C 396 405 414 423 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG T V SSASTKGP 450 459 468 477 441 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG V F P L A P S S K S T S G G T A 504 513 522 531 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA G C L V K D Y F P E P V T V S W N S 567 558 576 585 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GG2 G & L T S G V H T P P A V L O S S G

Fig. 16(C) (Sheet 1 of 3)

612 621 630 639 648 CTO TAC TOO OTO AGO AGO GTG GTG ACC GTG CCC TOO AGO AGO TTG GGO ACC CAG ___ ___ Y S L S S V V T V P S S S L G T Q ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA Y I C N V N H K P S N T K V D K K GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG V E P K S C D K T H T C C V E C P P TGC CCA GCA CCT GAA GGC AGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT PAPEGRLKIA A F N I Q T F GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG $\texttt{G} \quad \texttt{E} \quad \texttt{T} \quad \texttt{K} \quad \texttt{M} \quad \texttt{S} \quad \texttt{N} \quad \texttt{A} \quad \texttt{T} \quad \texttt{L} \quad \texttt{V}$ AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC SRYDIALVQEVRDSHLTA GTG SAG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC V E K L L D N L N Q D A P D T Y H Y GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG V V S E P L G R N S Y K E R Y L TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC E P C G N D T F N R E P A IVRFF TOO OGG TTO ACA GAG GTO AGG GAG TTT GOO ATT GTT COO CTG CAT GOG GOO COG S R F T E V R E F A I V P L H A A P

Fig. 16(C) (Sheet 2 of 3)

GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA 1269 1278 1287 1260 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC ___ ___ __ __ __ __ __ __ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ EKWGLEDV M L M G D F N A G C 1314 1323 1332 1341 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC Y V R P S O W S S I R L W T S P T 1368 1377 1386 1359 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT F Q W L I P D S A D T T A T P T H C 1422 1431 1440 1449 1413 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC A Y D R I V V A G M L L R G A V V P 1467 1476 1485 1494 1503 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG D'S A L P F N F Q A A Y G L S D Q L 1530 1539 1548 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' Q A I S D H Y P V E V M L K \star

Fig. 16(C) (Sheet 3 of 3)

pAS105

```
06-MAR-1995
            PAS105.DNA
                         1578 bp
                                    mRNA
                                                     PRI
            Humanised HMFG1 Fab'2 fused to human DNase I with SV40
DEFINITION
NLS (pAS105)
ACCESSION
NID
KEYWORDS
            DNase I.
            DNase I sequence is from assembled oligos (thus modified c/f
SOURCE
MHDNASE1.dna)
  ORGANISM
            Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  AUTHORS
            Recombinant human DNase I reduces the viscosity of cystic
  TITLE
fibrosis
            sputum
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  JOURNAL
  MEDLINE
            91067672
                                   442 q
                                            310 t
BASE COUNT
                353 a
                         473 c
ORIGIN
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAG GCGGGCCTGAA GATCGCAGCC
      781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
      841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
      901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
      961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
     1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
     1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
     1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
     1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
     1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
     1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
     1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
     1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
     1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA
     1561 AAGAAGCGCA AGGTTTGA
```

→ NLS

Fig. 17(A)

11

```
25-AUG-2000
LOCUS
            FDDNASE105
                         1578 BP SS-DNA
                                                    SYN
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
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     frag
                     /note="1 to 1578 of PAS105.dna [Split]"
     frag
                     721..780
                     /note="1 to 60 of 101/105linker"
                     join(721..>735,<736..>759,<760..>780)
     frag
                     /note="1 to 80 of 102linker [Split]"
                353 A
                         471 C
                                  443 G
                                           311 T
                                                       0 OTHER
BASE COUNT
ORIGIN
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC
      781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
      841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
      901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
      961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
     1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
     1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
     1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
     1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
     1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
     1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
     1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
     1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
     1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA
     1561 AAGAAGCGCA AGGTTTGA
```

Fig. 17(B)

```
1587 BP SS-DNA
                                                     SYN
                                                               29-AUG-2000
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LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
                     10..1587
     frag
                     /note="1 to 1578 of FdDNase105correct"
                     join(10..>729,<790..1587)
     frag
                     /note="1 to 1578 of PAS105.dna [Split]"
     frag
                     730..789
                     /note="1 to 60 of 101/105linker"
                     join(730..>744,<745..>768,<769..>789)
     frag
                     /note="1 to 80 of 102linker [Split]"
                         477 C
                                  445 G
                                           311 T
                354 A
BASE COUNT
ORIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
      781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCTCGTC
      841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAGAGAC
      901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
      961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTTC
     1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG
     1081 CCCTGCGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTTC
     1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCGGGGGA CGCAGTAGCC
     1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
     1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA
     1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
     1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
     1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTTAACTTCC AGGCTGCCTA TGGCCTGAGT
     1501 GACCAACTGG CCCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGGGGGGC
     1561 GGACCCAAAA AGAAGCGCAA GGTTTGA
```

Fig. 17(C)

45 54 27 18 3.6 ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC --- --- --- --- --- --- --- --- --- --- --- --- ---CIILFLVATATGVH 81 90 99 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA S Q V Q L V Q S G A E V K K P G A S 135 144 153 126 117 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG K V S C K A S G Y T F S A Y W I E 180 189 198 207 171 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT ___ ___ ___ W V R Q A P G K G L E W V G E I L P 252 270 234 243 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT S N N S R Y N E K F K G R V T V T 288 297 306 315 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG D T S T N T A Y M E L S S L R S 351 360 369 342 333 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC D T A V Y Y C A R S Y D F A W F A Y 405 414 423 396 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG G Q G T L V T V S S A S T K G P S 441 450 459 468 477 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG V F P L A P S S K S T S G G T A A L 531 513 522 504 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA G C L V K D Y F P E P V T V S W N S 567 576 585 549 558 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA A L T S G V H T F P A V L O S S G

Fig. 17(D) (Sheet 1 of 3)

Berte Mality of Selling (1984) - Fire Having I in a she se va

621 630 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG Y S L S S V V T V P S S S L G T O ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA Y I C N V N H K P S N T K V GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT V E P K S C D K T H T C P P C P A P GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG E G G L K I A A F N I Q T F G E T K ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC S N A T L V S Y I V Q I L S R Y D ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ A L V Q E V R D S H L T A V G K L 7973 6 CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG ___ L D N L N Q D A P D T Y H Y V V S E CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC P L G R N S Y K E R Y L F V Y R CAG GTG TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG O V S A V D S Y Y Y D D G C E P C G AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA D T F N R E P A I V R F F S R F T 1.152 GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA E V R E F A I V P L H A A P G D A V

Fig. 17(D) (Sheet 2 of 3)

GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC A E I D A L Y D V Y L D V Q E K W G 1251 1260 1269 1278 1287 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA ___ ___ ___ ___ L E D V M L M G D F N A G C S Y V R 1314 1323 1332 1341 1305 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG S Q W S S I R L W T S P T F Q W L 1368 1377 1386 1395 1359 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG I P D S A D T T A T P T H C A Y D R 1431 1440 1449 1413 1422 ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ I V V A G M L L R G A V V P D S A L 1476 1485 1494 1503 CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC P F N F Q A A Y G L S D Q L A Q A I 1530 1539 1548 1557 AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG D H Y P V E V M L K G G G P K K K 1575 CGC AAG GTT TGA 3' --- --- ---R K V *

Fig. 17(D) (Sheet 3 of 3)

pAS106

```
1596 bp
                                    mRNA
            PAS106.DNA
            Humanised HMFG1 Fab'2 fused to human DNase I with SV40
DEFINITION
NLS (pAS106)
ACCESSION
NID
KEYWORDS
            DNase I.
            DNase I sequence is from assembled oligos (thus modified c/f
SOURCE
MHDNASE1.dna)
  ORGANISM Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  AUTHORS
  TITLE
            Recombinant human DNase I reduces the viscosity of cystic
fibrosis
            sputum
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  JOURNAL
            91067672
  MEDLINE
                355 a
                         475 c
                                  452 g
                                           314 t
BASE COUNT
ORIGIN
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA
      781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
      841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
      901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
      961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
     1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
     1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
     1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
     1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
     1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
     1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC
     1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
     1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTTCCA GGCTGCCTAT
     1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
     1561 AAGGGGGGCG GACCCAAAAA GAAGCGCAAG GTTTGA
```

ightharpoonup NLS

Fig. 18(A)

//

```
25-AUG-2000
           FDDNASE106
                       1596 BP SS-DNA
                                                    SYN
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
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     frag
                     /note="1 to 1596 of PAS106.dna [Split]"
                     721..798
     frag
                     /note="1 to 78 of 102/106linker"
                                  452 G
                                                      0 OTHER
                                           315 T
                355 A
                         474 C
BASE COUNT
ORIGIN
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       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGGAGCGGC
      781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
      841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
      901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
      961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
     1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
     1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
     1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
     1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
     1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
     1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC
     1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
     1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTTCCA GGCTGCCTAT
     1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
     1561 AAGGGGGGC GACCCAAAAA GAAGCGCAAG GTTTGA
```

Fig. 18(B)

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29-AUG-2000
                                                    SYN
LOCUS
            FDDNASE106
                       1605 BP SS-DNA
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
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     frag
                     /note="1 to 1596 of FdDNase106correct"
                     join(10..>729,<808..1605)
     frag
                     /note="1 to 1596 of PAS106.dna [Split]"
                     730..807
     frag
                     /note="1 to 78 of 102/106linker"
                356 A
                                  454 G
                                           315 T
                                                      0 OTHER
BASE COUNT
ORIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
      781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTTGGGGA GACCAAGATG
      841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG
      901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT
      961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT
     1021 AAGGAGCGCT ACCTGTTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC
     1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC
     1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAGG GAGTTTGCCA TTGTTCCCCT GCATGCGGCC
     1201 CCGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG
     1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGCGACTTCA ATGCGGGCTG CAGCTATGTG
     1321 AGACCCTCCC AGTGGTCATC CATCCGCCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC
     1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT
     1441 GCAGGGATGC TGCTCCGAGG GGCCGTTGTT CCCGACTCGG CTCTTCCCTT TAACTTCCAG
     1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG
     1561 GTGATGCTGA AGGGGGGGGG ACCCAAAAAG AAGCGCAAGG TTTGA
```

Fig. 18(C)

		9			18			27			36			45			-f54
ATG	GGA	TGG	AGC	TGT	ATC	АТС	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	ÇAC
М	G	w	S	С	I	I	L	F	L	V	A	T	A	T	G	v	Н
		63			72			81			90			99			108
TCC	CAG		CAG	CTG							GTG	AAA	AAG		GGG	GCC	
								 G		 E	 V		 К	 P	 G	 A	 S
S	Q	V	Q	L	V	Q	5	G	A	£	V	V	K	£	G		3
CTV	N N C	117	#\C	™ CC	126	CCT	ጥረጥ	135 CCC	ጥልር	ACC.	144 TTC	ልርጥ	CCC	153	ጥርር	ፈ ጥል	162 GAG
	AAG																
V	K	V	S	С	K	A	S	G	Y	T	F	S	A	Y	W	I	Ē
		171			180			189			198			207			216
TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	TTA	ATT	CCT
W	V	R	Q	A	P	G	K	G	L	E	W	v	G	E	I	L	₽
		225			234			243			252			261			270
GGA	AGT		TAA	TCT		TAC	AAT		AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
 G	 S	 N	n	 S	 R	 У	 N	 E		 F		 G	 R	 V	т	v	т
														225			224
AGA	GAC	279 ACA		ACA	288 AAC		GCC			GAG	306 CTC		AGC	315 CTG		TCT	324 GAG
R	D	T	S	T	N	T	A	Y	М	E	L	S	S	L	R	S	E
C L C	X C X	333	CTC	ጥአጥ	342	መረጥ	CCA	351		ሞአር	360 GAC	ششش	CCC	369	ሙጥጥ	CCT	378 TAC
D	T	A	V	Y	Y	С	A	R	S	Y	D	F	А	W	F	A	Y
		387			396									423			432
TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG 	GGC	CCA	TCG
W	G	Q	G	T	L	V	T	V	s	s	A	S	\mathbf{T}	K	G	P	S
		441			450			459			468			477			486
GTC	TTC					TCC					TCT					GCC	CTG
v	F	P									s					A	L
		495			504			513			522			531			540
GGC	TGC			AAG						CCG	GTG					AAC	
- <i></i> -	 C	 L	 V	 K	 D	 Y	 F		 E		 V			 S			 S
-	-																
GGC	GCC	549 CTG		: AGC			CAC			: CCG	576 GCT	GTC		585 CAG		TCA	594 GG4
G	A	I,	Υ	S	G	V	Н	Т	F	Þ	Α	V	L	Q	S	S	G

Fig. 18(D)

(Sheet 1 of 3)

CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K V D K K GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG $\begin{smallmatrix} V \end{smallmatrix} \ \, \begin{smallmatrix} E \end{smallmatrix} \ \, P \hspace{1mm} K \hspace{1mm} S \hspace{1mm} C \hspace{1mm} D \hspace{1mm} K \hspace{1mm} T \hspace{1mm} H \hspace{1mm} T \hspace{1mm} C \hspace{1mm} C \hspace{1mm} V \hspace{1mm} E \hspace{1mm} C \hspace{1mm} P \hspace{1mm} P \hspace{1mm} \\ \begin{smallmatrix} E \end{smallmatrix} \ \, \begin{matrix} E \hspace{1mm} C \hspace{1mm} P \hspace{1mm} P \hspace{1mm} \\ \end{smallmatrix} \ \, \begin{matrix} E \hspace{1mm} C \hspace{1mm} P \hspace{1mm} P \hspace{1mm} \\ \end{smallmatrix} \ \, \begin{matrix} E \hspace{1mm} C \hspace{1mm} P \hspace{1mm} P \hspace{1mm} P \hspace{1mm} \\ \end{smallmatrix} \ \, \begin{matrix} E \hspace{1mm} C \hspace{1mm} P \hspace{1mm} P \hspace{1mm} P \hspace{1mm} \end{matrix}$ TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG PAPEGSGGLKIAA ACA TIT GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG T F G E T K M S N A T L V S Y I V Q ATC CTG AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG I L S R Y D I A L V Q E V R D S H L ACT GCC GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT T A V G K L L D N L N Q D A P D T Y CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG Y V V S E P L G R N S Y K E R Y L TTC GTG TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT --- --- --- --- --- --- --- --- --- --- --- --- --- ---A V D S Y Y Y D D V Y R P D Q V S GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG GCEPCGNDTFN R E TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG FFSRFTEVREFAIVPL## 1233 1242

Fig. 18(D) *(Sheet 2 of 3)*

- 2 -

GCC CCG GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC 1'AC CTG GAT ___ ___ __ __ __ __ __ __ __ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ P G D A V A E I D A L 1260 1269 1278 1287 GTC CAA GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG O E K W G L E D V M L M G D F N A 1332 1305 1314 1323 1341 GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC G C S Y V R P S Q W S S I R L W T S 1368 1377 1386 1395 1359 CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG --- --- --- --- --- --- --- --- --- --- --- --- --- ---P T F Q W L I P D S A D T T A T P T 1431 1440 1449 1422 CAC TGT GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT ___ H C A Y D R I V V A G M L L R G A V 1476 1485 1494 GTT CCC GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC ___ ___ __ __ __ __ __ __ __ __ __ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ __ 1530 1539 1548 1557 1521 CAA CTG GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---Q L A Q A I S D H Y P V E V M L K G 1584 1593 GGC GGA CCC AAA AAG AAG CGC AAG GTT TGA 3' G G P K K K R K V *

Fig. 18(D)

(Sheet 3 of 3)

pAS107

```
06-MAR-1995
            PAS107.DNA
                         1590 bp
                                    mRNA
                                                     PRI
LOCUS
            Humanised HMFG1 Fab'2 fused to human DNase I with SV40
DEFINITION
NLS (pAS107)
ACCESSION
NID
KEYWORDS
            DNase I.
            DNase I sequence is from assembled oligos (thus modified c/f
SOURCE
MHDNASE1.dna)
            Homo sapiens
  ORGANISM
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  AUTHORS
            Recombinant human DNase I reduces the viscosity of cystic
  TITLE
fibrosis
            sputum
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  JOURNAL
            91067672
  MEDLINE
BASE COUNT
                354 a
                         474 c
                                   448 g
                                            314 t
ORIGIN
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       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACA<u>TGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCGGG</u>CTG
      781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
      841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
      901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
      961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
     1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
     1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
     1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
     1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
     1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
     1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
     1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
     1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
     1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGGGG
```

_NLS

1561 GGCGGACCCA AAAAGAAGCG CAAGGTTTGA

Fig. 19(A)

```
SYN
                                                              25-AUG-2000
            FDDNASE107
                       1590 BP SS-DNA
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
FEATURES
                     Location/Qualifiers
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                     join(721..>771,<772..792)
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                                           315 T
BASE COUNT
                354 A
                         473 C
                                  448 G
                                                      0 OTHER
ORIGIN
        1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
       61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
      121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
      181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
      241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
      301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
      361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
      421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
      481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
      541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
      601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
      661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
      721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCGGGCTG
      781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
      841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
      901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
      961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
     1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
     1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
     1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
     1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
     1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
     1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
     1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
     1441 CGAGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
     1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGGGG
     1561 GGCGGACCCA AAAAGAAGCG CAAGGTTTGA
```

Fig. 19(B)

```
FDDNASE107
                       1599 BP SS-DNA
LOCUS
                                                    SYN
                                                              29-AUG-2000
DEFINITION
ACCESSION
KEYWORDS
SOURCE
FEATURES
                     Location/Qualifiers
                     10..1599
     frag
                     /note="1 to 1590 of FdDNase107correct"
                     join(10..>729,<802..1599)
     frag
                     /note="1 to 1590 of PAS107.dna [Split]"
                     730..801
     frag
                     /note="1 to 72 of 103/107linker"
                     join(730..>780,<781..801)
     frag
                     /note="1 to 78 of 102linker [Split]"
                355 A
                                           315 T
                                  450 G
BASE COUNT
                         479 C
                                                      0 OTHER
ORIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
      121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
      181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
      241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
      301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
      541 TGGAACTCAG GCGCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
      781 GGCGGGCTGA AGATCGCAGC CTTCAACATC CAGACATTTG GGGAGACCAA GATGTCCAAT
      841 GCCACCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG
      901 GAGGTCAGAG ACAGCCACCT GACTGCCGTG GGGAAGCTGC TGGACAACCT CAATCAGGAC
      961 GCACCAGACA CCTATCACTA CGTGGTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG
     1021 CGCTACCTGT TCGTGTACAG GCCTGACCAG GTGTCTGCGG TGGACAGCTA CTACTACGAT
     1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAGGTTC
     1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTTC CCCTGCATGC GGCCCCGGGG
     1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
     1261 GGCTTGGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
     1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
     1381 AGCGCTGACA CCACAGCTAC ACCCACGCAC TGTGCCTATG ACAGGATCGT GGTTGCAGGG
     1441 ATGCTGCTCC GAGGGGCCGT TGTTCCCGAC TCGGCTCTTC CCTTTAACTT CCAGGCTGCC
     1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG
     1561 CTGAAGGGGG GCGGACCCAA AAAGAAGCGC AAGGTTTGA
```

Fig. 19(C)

ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC M G W S C I I L F L V A T A T G V H TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA _________ S Q V Q L V Q S G A E V K K P G A S GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG V K V S C K A S G Y T F S A Y W I E TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT $\hbox{\tt W} \quad \hbox{\tt V} \quad \hbox{\tt R} \quad \hbox{\tt Q} \quad \hbox{\tt A} \quad \hbox{\tt P} \quad \hbox{\tt G} \quad \hbox{\tt K} \quad \hbox{\tt G} \quad \hbox{\tt L} \quad \hbox{\tt E} \quad \hbox{\tt W} \quad \hbox{\tt V} \quad \hbox{\tt G}$ GGA AGT AAT AAT TOT AGA TAC AAT GAG AAG TTO AAG GGO CGA GTG ACA GTO ACT $\hbox{\tt G} \quad \hbox{\tt S} \quad \hbox{\tt N} \quad \hbox{\tt N} \quad \hbox{\tt S} \quad \hbox{\tt R} \quad \hbox{\tt Y} \quad \hbox{\tt N} \quad \hbox{\tt E} \quad \hbox{\tt K} \quad \hbox{\tt F} \quad \hbox{\tt K} \quad \hbox{\tt G} \quad \hbox{\tt R} \quad \hbox{\tt V} \quad \hbox{\tt T} \quad \hbox{\tt V}$ AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG R D T S T N T A Y M E L S S L R S E GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG ___ ___ ___ ___ W G Q G T L V T V S S A S T K G P S GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG V F P L A P S S K S T S G G T A A L GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA V T V S W N S K D Y F P E P GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA V A 9 T H V L Q G A L T S

Fig. 19(D) (Sheet 1 of 3)

612 621 630 639 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG L Y S L S S V V T V P S S S L G T Q ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K V D K K 729 738 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG V E P K S C D K T H T C C V E C P P TGC CCA GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT PAPEGGLKIAAFNIQTF GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG M S N A T L V S Y AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC RYDIALVQEVRD GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC G K L L D N L N Q D A P D GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG V S E P L G R N S Y K E R TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC R P D Q V S A V D S Y Y Y GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC P C G N D T F N R E P A I V R TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG RFTEVREFAIVPLHAAP

Fig. 19(D) (Sheet 2 of 3)

GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA G D A V A E I D A L Y D V Y L D V Q 1269 1278 1287 1260 1251 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC --- --- --- --- --- --- --- --- --- --- --- --- --- ---E K W G L E D V M L M G D F N A G C 1314 1323 1332 1341 1305 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC S Y V R P S Q W S S I R L W T S P T 1368 1377 1386 1395 1359 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT F Q W L I P D S A D T T A T P T H C 1440 1449 1458 1431 1422 1413 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC RIVVAGMLLRGAVVP 1503 1467 1476 1485 1494 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG --- --- --- --- --- --- --- --- --- --- --- --- --- ---D S A L P F N F Q A A Y G L S D Q L 1530 1539 1548 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA A Q A I S D H Y P V E V M L K G G G 1584 1575 CCC AAA AAG AAG CGC AAG GTT TGA 3' P K K K R K V *

Fig. 19(D) (Sheet 3 of 3)

Mammalian expression of humanised HMFG1-D Nase constructs

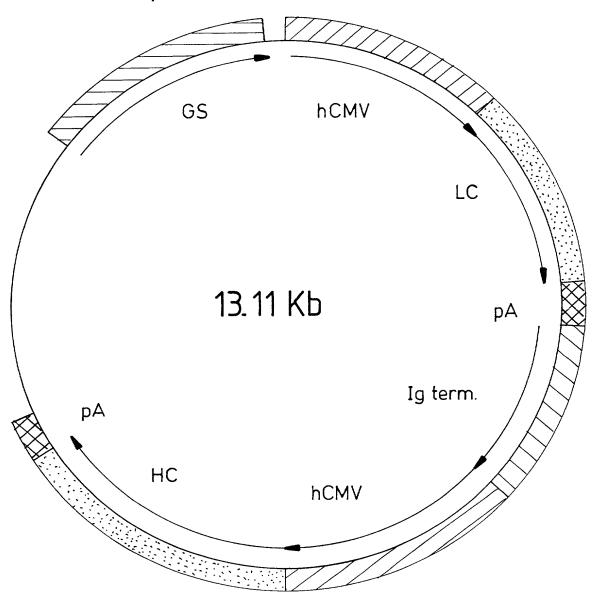


Fig. 20

Immuno-precipitation of metabolically labelled transient transfectants

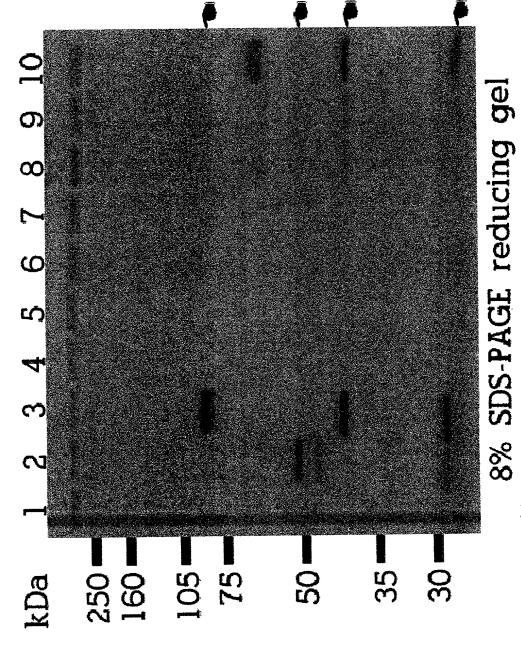


Fig. 21(4)

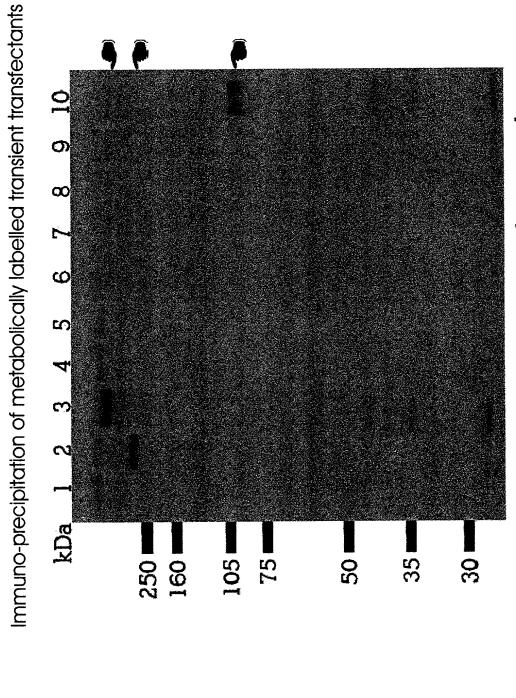
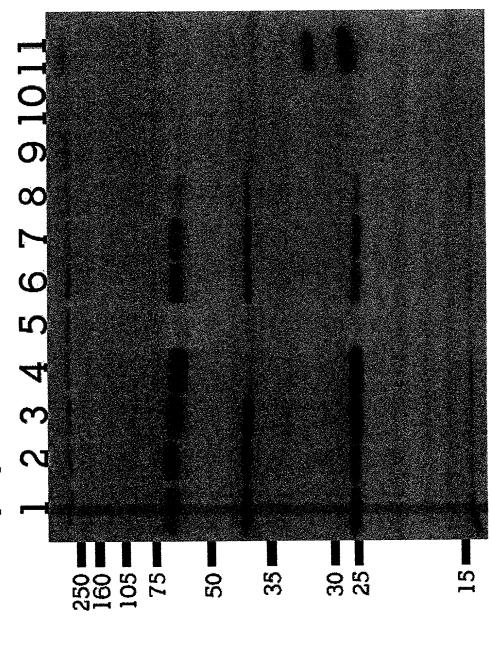


Fig. 21(B)

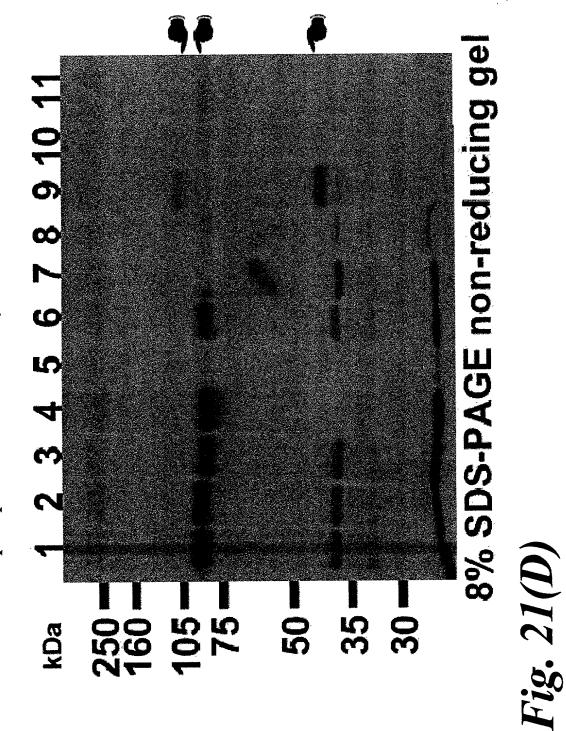
8% SDS-PAGE non-reducing gel

Immuno-precipitation of metabolically labelled transient transfectants



10% SDS-PAGE reducing gel Fig. 21(C)

Immuno-precipitation of metabolically labelled transient transfectants



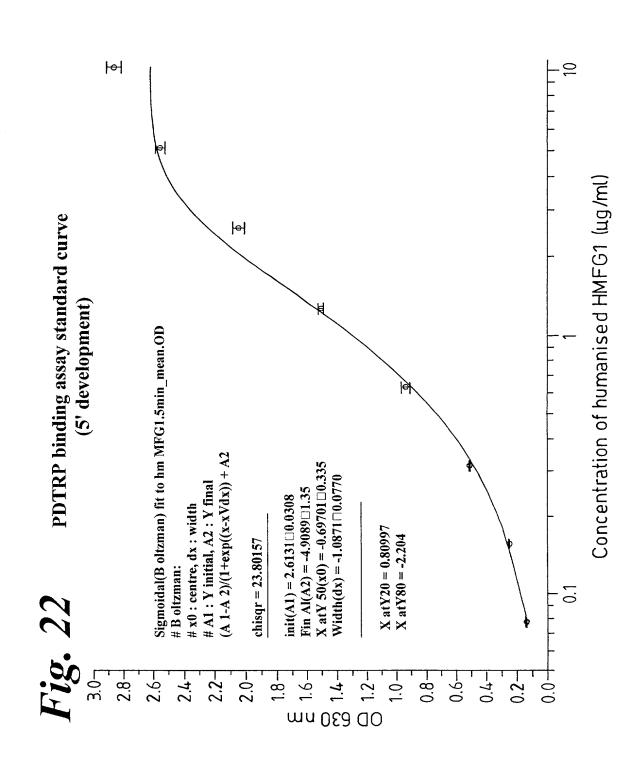
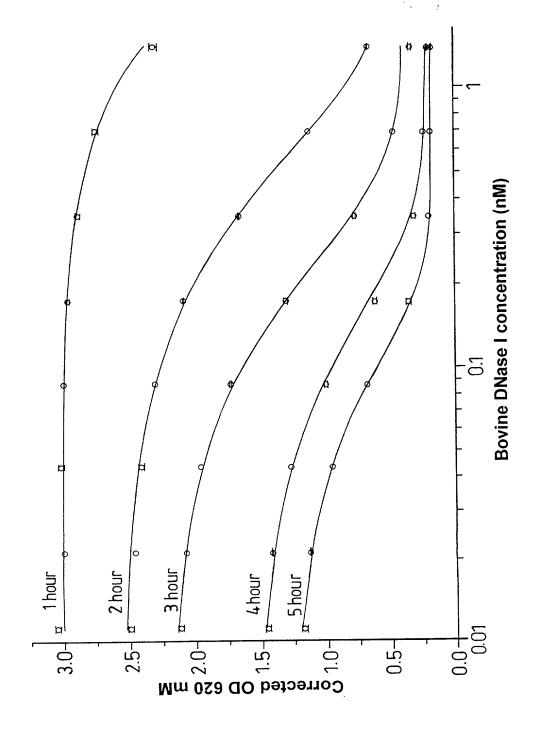
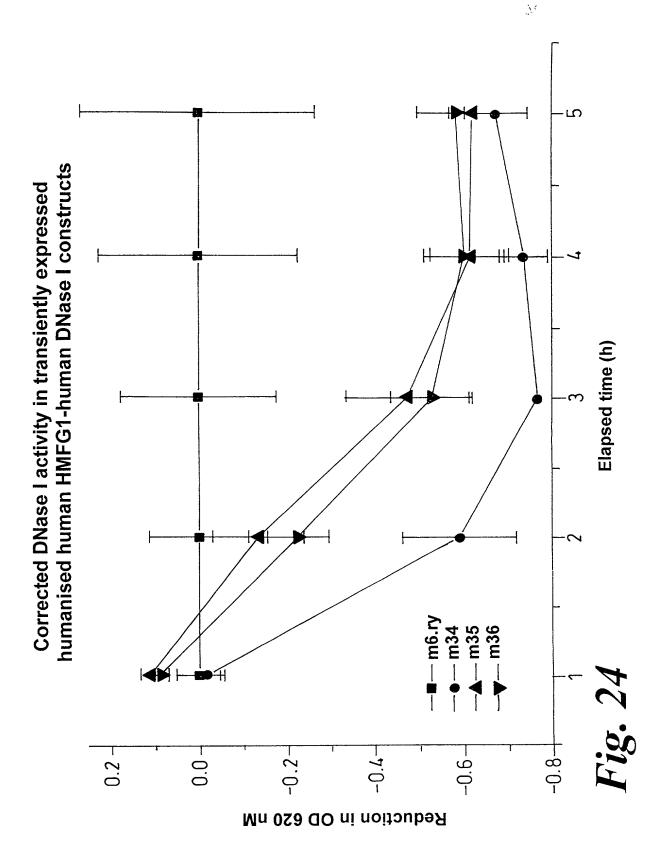


Fig. 23

Corrected bovine DNase I standard curves at various time points





S Corrected DNase I activity in transiently expressed humanised HMFG1 F(ab')2-human DNase I fusions Elapsed time (h) m103 mb41 -m102____m_101 Reduction in OD 620nm

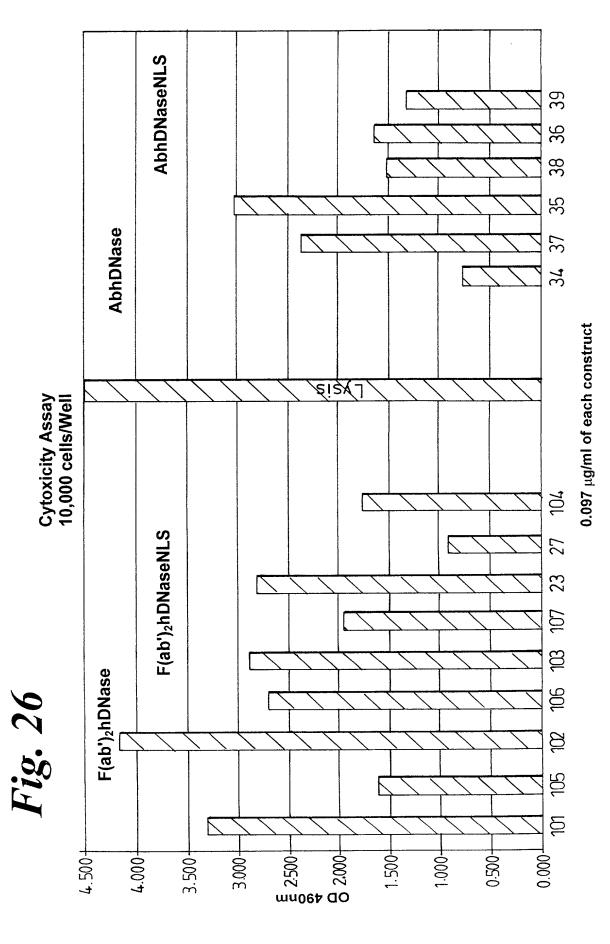
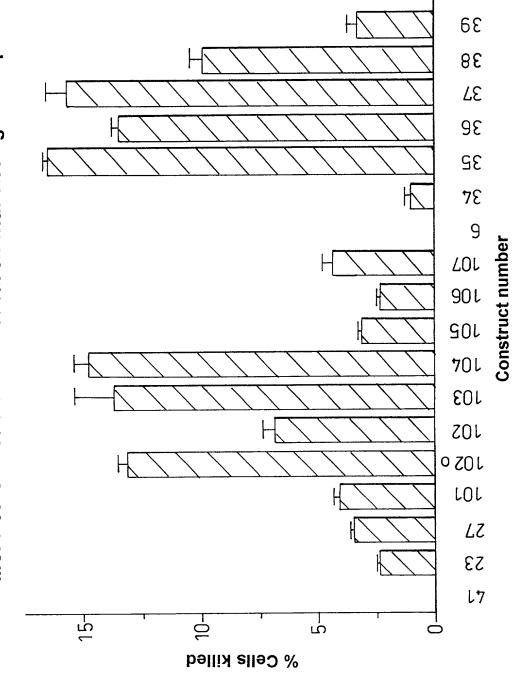
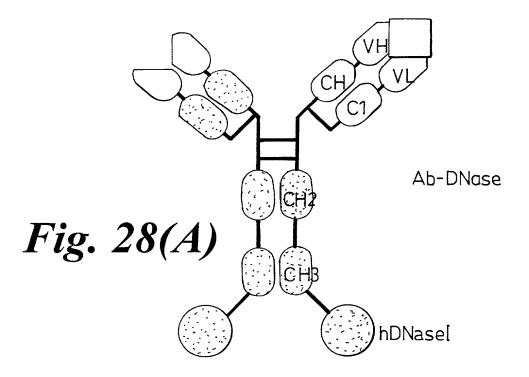


Fig. 27







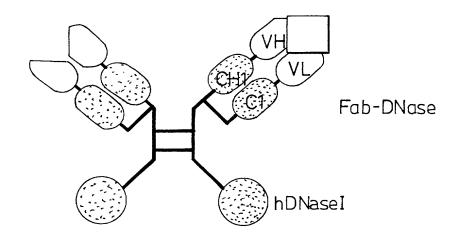
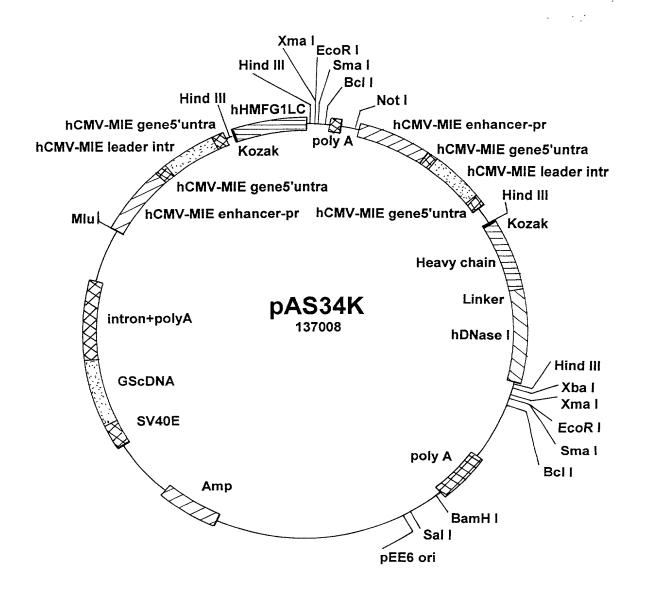
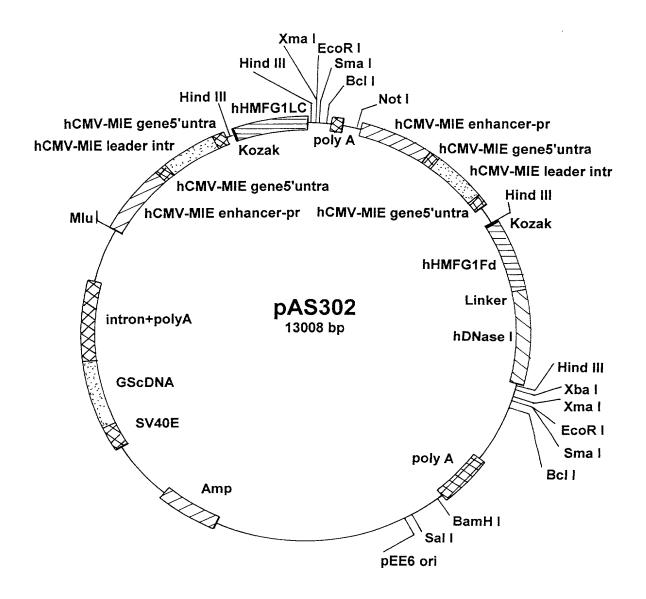


Fig. 28(B)



Ab-DNase

Fig. 29



Fab-DNase

Fig. 30

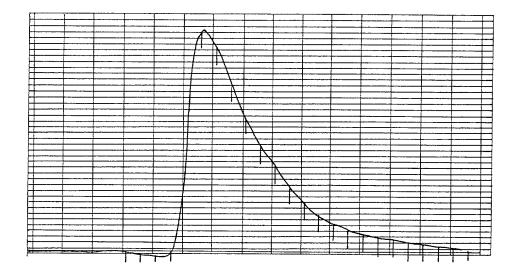


Fig. 31(A)

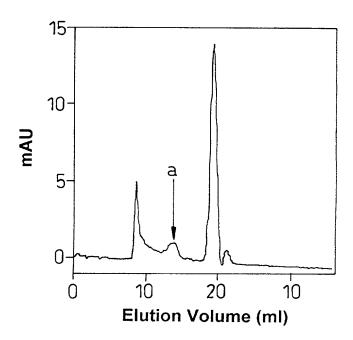
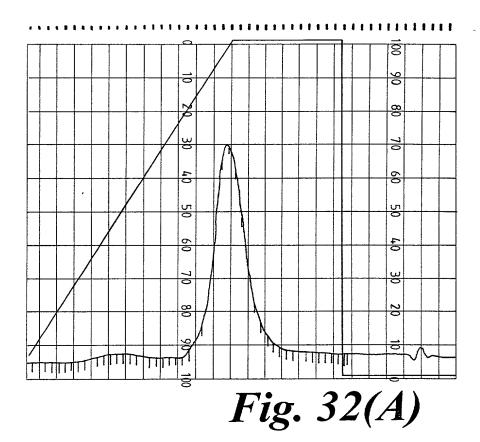


Fig. 31(B)



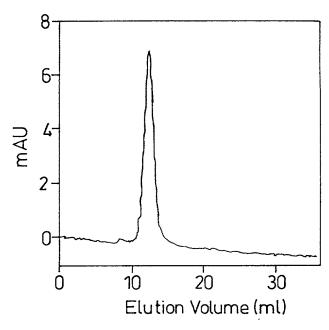
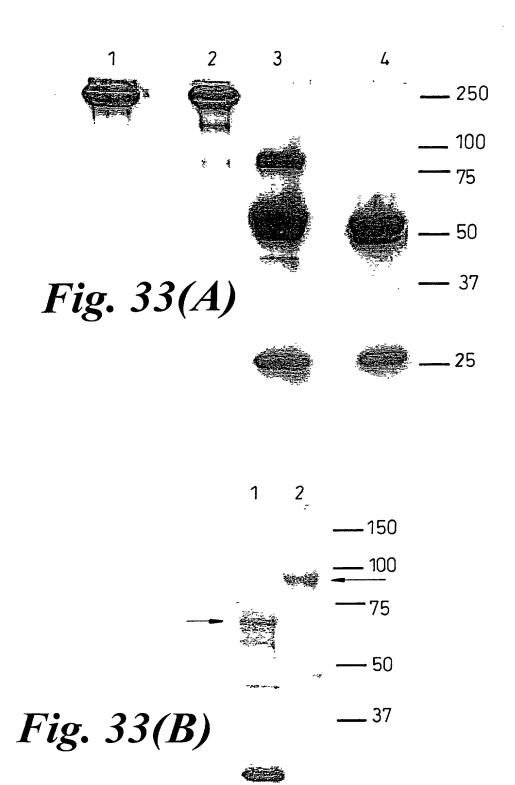


Fig. 32(B)



Bovine DNase I standard curves at various time points

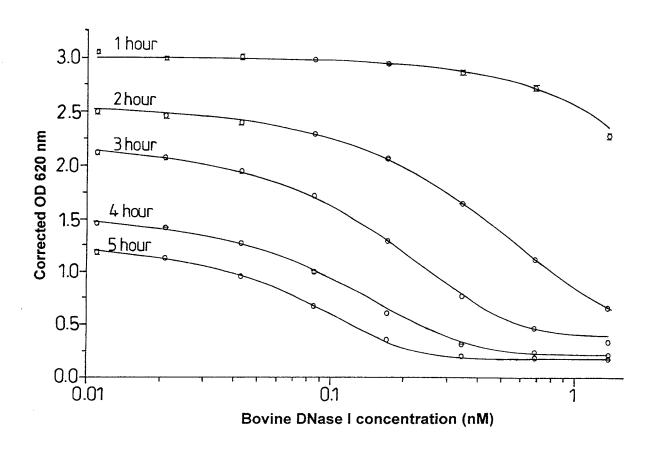


Fig. 34(A)

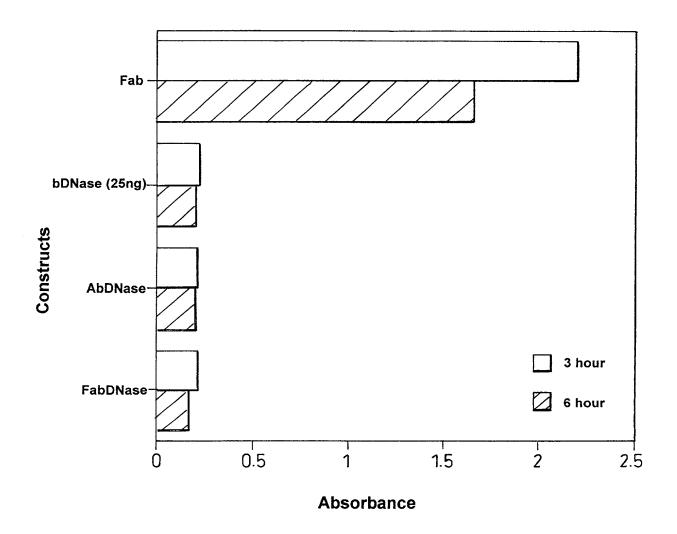


Fig. 34(B)

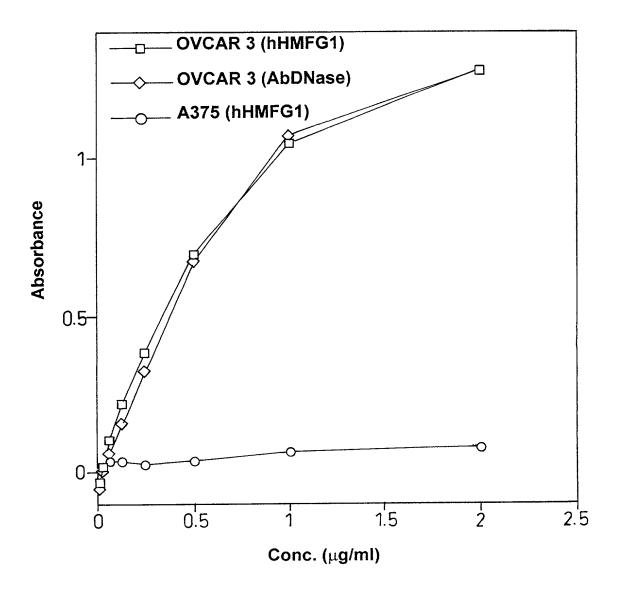


Fig. 35(A)

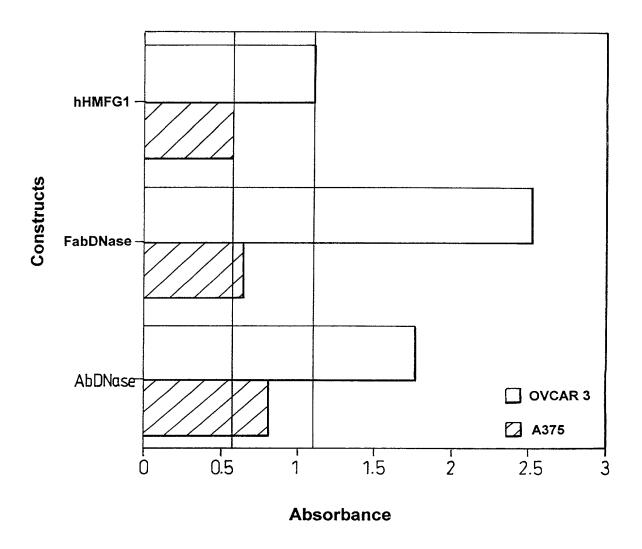


Fig. 35(B)